

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on:

June 9, 2004, 18:10:48 ; Search time 19489 seconds

(without alignments)

7078.910 Million cell updates/sec

Title:

US-10-072-077A-1

Perfect score:

3183

Sequence:

1 gatatatctcttttatattca.....tatgttactagatcgaattc 3183

Scoring table:

IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched:

3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters:

6940544

Minimum DB seq length:

0

Maximum DB seq length:

200000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_on:\*

5: gb\_ovr:\*

6: gb\_pat:\*

7: gb\_Ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vir:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_on:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vi:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pln:\*

35: em\_htg\_rod:\*

36: em\_htg\_mam:\*

37: em\_htg\_vrt:\*

38: em\_sy:\*

39: em\_htgo\_hum:\*

40: em\_htgo\_mus:\*

41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	% Match	DB ID	Description
1	3183	100.0	3183	6	I75096 Sequence 1
2	3171	99.6	3182	6	AR201516 Sequence
3	2182.4	.68.6	3659	8	U37336 Agrobacteri
4	2075.8	.65.2	59648	8	AB016870 Agrobacteri
5	733.4	.23.0	1296	1	K02000 Ti plasmid
6	733.4	.23.0	1988	1	X00010 Agrobacteri
7	733.4	.23.0	24595	1	X00493 Agrobacteri
8	733.4	.23.0	24595	6	E00404 Ti plasmid
9	733.4	.23.0	24595	6	E00546 DNA fragmen
10	733.4	.23.0	24595	6	AR364803 Sequence
11	733.4	.23.0	24595	6	X00639 Agrobacteri
12	733.4	.23.0	194140	1	AB242881 Agrobacte
13	709	.22.3	709	6	I75097 Sequence 2
14	709	.22.3	709	6	AR201517 Sequence
15	636.6	.20.0	1983	1	ATTMRPTI
16	636.6	.20.0	206479	1	AB016312 Method of
17	635	.19.9	9931	1	AF242881 Agrobacte
18	635	.19.9	10377	1	AE007927 Agrobacte
19	633.4	.19.9	29524	1	AE009419 Agrobacte
20	630.2	.19.8	1997	1	AJ237588 Agrobacte
21	615.2	.19.3	1382	1	AB025109 Agrobacte
22	615.2	.19.3	10200	1	PLATIPTG X17428 Plasmid Ti
23	615.2	.19.3	15463	1	X56185 A.tumefaci
24	614.4	.19.3	14960	1	U83987 Agrobacteri
25	585.8	.18.4	2724	1	AB032122 Agrobacte
26	560.2	.17.6	6482	1	X77327 A.vitis iaa
27	546.6	.17.2	1919	1	X14410 Agrobacteri
28	536.4	.16.9	3017	6	AX03934 Sequence
29	536	.16.8	2722	6	AX039930 Sequence
30	536	.16.8	2722	6	AX039931 Sequence
31	536	.16.8	5622	6	AX039929 Sequence
32	354.2	.11.1	420	1	TIPTMR M34934 Plasmid pTi
33	344.4	.10.8	584	6	I18499 Sequence 2
34	262.8	.8.3	7599	6	AX063413 Sequence
35	261.8	.8.2	4280	6	AX063410 Sequence
36	261.8	.8.2	4309	6	AX063412 Sequence
37	257.2	.8.1	1829	6	A26453 Recombinant
38	257.2	.8.1	116753	6	I16753 Sequence 17
39	257.2	.8.1	1863	6	A32909 Chimeric en
40	257.2	.8.1	1863	6	A40108 Sequence 16
41	257.2	.8.1	1863	6	AR022666 Sequence
42	257.2	.8.1	1863	6	AR029592 Sequence
43	257.2	.8.1	4284	6	A40106 Sequence 14
44	257.2	.8.1	4284	6	AR022664 Sequence
45	257.2	.8.1	10436	12	AY297842 Transform

## ALIGNMENTS

RESULT 1  
I75096 LOCUS I75096 DEFINITION Sequence 1 from patent US 5689042. ACCESSION I75096 VERSION I75096.1 GI:3011237 KEYWORDS SOURCE Unknown. ORGANISM Unclassified. REFERENCES 1 (bases 1 to 3183)  
Amasino, R.M. and Gan, S.  
TITLE Transgenic plants with altered senescence characteristics  
JOURNAL Patent: US 5689042-A1 1B-NOV-1997;  
FEATURES Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

source	Query Match	Best Local Similarity	Score	DB	Length
ORIGIN	1. .3183 /organism="unknown" /mol_type="unassigned DNA"	100.0%	3183	6	3183
Matches 3183; Conservative	0;	Mismatches	0;	Indels	0;
Db	QY	1 GATATCTCTTTATTCACAACTAACATAAGTGGAGATATGTTGAGAGAGAACACTATT	60		
Db	QY	1 GATATCTCTTTATTCACAACTAACATAAGTGGAGATATGTTGAGAGAGAACACTATT	60		
Db	QY	61 CTCGTGGAGCACCGAGCTGTTTATTAGAAACCCGATTGGTATTGACTGAGAC	120		
Db	QY	61 CTCGTGGAGCACCGAGCTGTTTATTAGAAACCCGATTGGTATTGACTGAGAC	120		
Db	QY	121 AAAAGTAAATC GTT GAT GTT AAT TAA ATT AGT TT CAT CAC GTT CGA AAAA	180		
Db	QY	121 AAAAGTAAATC GTT GAT GTT AAT TAA ATT AGT TT CAT CAC GTT CGA AAAA	180		
Db	QY	181 AAATGATTGTTATCAGCTAATAGCATGATCTAAATTGTTTTGACACCCCTT	240		
Db	QY	181 AAATGATTGTTATCAGCTAATAGCATGATCTAAATTGTTTTGACACCCCTT	240		
Db	QY	241 TTTCCTCTTGGTTCTAACATTAGCATAGCTAAATAGCATGATCTAAATTGTTTGACACCCCTT	300		
Db	QY	241 TTTCCTCTTGGTTCTAACATTAGCATAGCTAAATAGCATGATCTAAATTGTTTGACACCCCTT	300		
Db	QY	301 ATTAAACAAATTTCAAGTTTATACGAAACTTGTGTTTAATGAAAAGCT	360		
Db	QY	301 ATTAAACAAATTTCAAGTTTATACGAAACTTGTGTTTAATGAAAAGCT	360		
Db	QY	361 GAATAGTGTATTGAATTAGTTAGCAATACTCAATATGATCAATGATGTATAT	420		
Db	QY	421 ATGAACTCA GTGTTATACAGCTATTAAATACCGATCATGAGTGT	480		
Db	QY	421 ATGAACTCA GTGTTATACAGCTATTAAATACCGATCATGAGTGT	480		
Db	QY	481 AAAAGTGTCAAATATGACATGAAGCGTTTGCCCTACCGGTATCGAGTTAGGTT	540		
Db	QY	481 AAAAGTGTCAAATATGACATGAAGCGTTTGCCCTACCGGTATCGAGTTAGGTT	540		
Db	QY	541 GGATCTCTCAA GAATATTTGGCCATATTAGTTATGGCTTAAGC GTT TGCAA	600		
Db	QY	541 GGATCTCTCAA GAATATTTGGCCATATTAGTTATGGCTTAAGC GTT TGCAA	600		
Db	QY	601 GAGACGAGGAAGATGGCTCAAGTAACAAACAGACACTCGTAACTCGTA	660		
Db	QY	601 GAGACGAGGAAGATGGCTCAAGTAACAAACAGACACTCGTAACTCGTA	660		
Db	QY	661 CTTGGTAGCAACTCGATTATTGCCAGTAACAAACAGACACTCGTAACTCGTA	720		
Db	QY	661 CTTGGTAGCAACTCGATTATTGCCAGTAACAAACAGACACTCGTAACTCGTA	720		
Db	QY	721 TCGTTATTAGTTGACTCGTACCTTGGTAAAGTGTATAGTTGCTA	780		
Db	QY	721 TCGTTATTAGTTGACTCGTACCTTGGTAAAGTGTATAGTTGCTA	780		
Db	QY	781 TGTGTTCATGAGGTGATTTGATTAACATTTGCCACGCTCGTAAGTTGGTA	840		
Db	QY	781 TGTGTTCATGAGGTGATTTGATTAACATTTGCCACGCTCGTAAGTTGGTA	840		
Db	QY	841 TAACAAGTTATAGTTTTTATAACATTTGCCACGCTCGTAAGTTGGTA	900		
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Db	QY	901 TTACACCGCATTTCCCTGTACAGAAATCATAATTATTTACTCCAGT	960		
Db	QY	901 TTACACCGCATTTCCCTGTACAGAAATCATAATTATTTACTCCAGT	960		
Db	QY	2041 AAAATGCTTGGATCACTCATGACATTACATCAACCTTA	2100		

Db	3121 TATGGCGCGCAACTGGGATAATTATCGCGCGGGTGTACATCTATGTACTAGATCGAA 3180	QY	3181 TTC 3183
QY	2041 AAAATGCTTGTGATCACTCATGTGAACATTACATCAAACCTA 2100	Db	3181 TTC 3183
Db	2101 TTTCACTATAAACCCATCTCAGTACCTCTGAAGTAATCAAATTAGGCAAAGT 2160	QY	2101 TTTCACTATAAACCCATCTCAGTACCTCTGAAGTAATCAAATTAGGCAAAGT 2160
Db	2161 CATTAACTTCTAAACCATGGACCCCTGCATCTAATTTCGGTCCAACCTGCACAGGA 2220	QY	2161 CATTAACTTCTAAACCATGGACCCCTGCATCTAATTTCGGTCCAACCTGCACAGGA 2220
Db	2221 AAGACACGACGCCGATAGCTCTGCCAGCAGACAGGGCTCCAGTCCTCGCTGAT 2280	QY	2221 AAGACACGACGCCGATAGCTCTGCCAGCAGACAGGGCTCCAGTCCTCGCTGAT 2280
Db	2281 CGGGTCCAATCGTGTCTCAACTATCAACCGGAAAGGGGACCAACAGTGGAAACTG 2340	QY	2281 CGGGTCCAATCGTGTCTCAACTATCAACCGGAAAGGGGACCAACAGTGGAAACTG 2340
Db	2341 AAAGGAACGACCGGTCTACCTGGATGATCGGCCTCTGGGGTGGAGGTATCATCGCAGG 2400	QY	2341 AAAGGAACGACCGGTCTACCTGGATGATCGGCCTCTGGGGTGGAGGTATCATCGCAGG 2400
Db	2341 AAAGGAACGACCGGTCTACCTGGATGATCGGCCTCTGGGGTGGAGGTATCATCGCAGG 2400	QY	2341 AAAGGAACGACCGGTCTACCTGGATGATCGGCCTCTGGGGTGGAGGTATCATCGCAGG 2400
Db	2401 AAGCAAGCTCATAGGGTGTGAGGGGAGGTATAATCATGAGGCCAACGGGGGCTT 2460	QY	2401 AAGCAAGCTCATAGGGTGTGAGGGGAGGTATAATCATGAGGCCAACGGGGGCTT 2460
Db	2401 AAGCAAGCTCATAGGGTGTGAGGGGAGGTATAATCATGAGGCCAACGGGGGCTT 2460	QY	2401 AAGCAAGCTCATAGGGTGTGAGGGGAGGTATAATCATGAGGCCAACGGGGGCTT 2460
Db	2461 ATTCTTGAGGGGATCCACCTCGTTGCTCAACTGCATGGGGCGAACACAGCTATTGGAGT 2520	QY	2461 ATTCTTGAGGGGATCCACCTCGTTGCTCAACTGCATGGGGCGAACACAGCTATTGGAGT 2520
Db	2461 ATTCTTGAGGGGAGGATCCACCTCGTTGCTCAACTGCATGGGGCGAACACAGCTATTGGAGT 2520	QY	2461 ATTCTTGAGGGGAGGATCCACCTCGTTGCTCAACTGCATGGGGCGAACACAGCTATTGGAGT 2520
Db	2521 GCAGATTTCGTTGGCATATTATCGCCACAAGTTACCCGACCAAGAGACCTTCATGAAA 2580	QY	2521 GCAGATTTCGTTGGCATATTATCGCCACAAGTTACCCGACCAAGAGACCTTCATGAAA 2580
Db	2521 GCAGATTTCGTTGGCATATTATCGCCACAAGTTACCCGACCAAGAGACCTTCATGAAA 2580	QY	2521 GCAGATTTCGTTGGCATATTATCGCCACAAGTTACCCGACCAAGAGACCTTCATGAAA 2580
Db	2581 GCGGCCAAGGCCAGAGTTAACCGAGTGTGCAACCCGCTGAGGCCATTCTTCAA 2640	QY	2581 GCGGCCAAGGCCAGAGTTAACCGAGTGTGCAACCCGCTGAGGCCATTCTTCAA 2640
Db	2581 GCGGCCAAGGCCAGAGTTAACCGAGTGTGCAACCCGCTGAGGCCATTCTTCAA 2640	QY	2581 GCGGCCAAGGCCAGAGTTAACCGAGTGTGCAACCCGCTGAGGCCATTCTTCAA 2640
Db	2641 GAGTTGGTTATCTTGGATGAACCTCGGCTGAGGCCATTCTGGAAAGAGATCGATGGA 2700	QY	2641 GAGTTGGTTATCTTGGATGAACCTCGGCTGAGGCCATTCTGGAAAGAGATCGATGGA 2700
Db	2641 GAGTTGGTTATCTTGGATGAACCTCGGCTGAGGCCATTCTGGAAAGAGATCGATGGA 2700	QY	2641 GAGTTGGTTATCTTGGATGAACCTCGGCTGAGGCCATTCTGGAAAGAGATCGATGGA 2700
Db	2701 TATCGATATGCCATGTGTGCTAGCCAGAACAGATCACGGCAGATATGCTATTGCA 2760	QY	2701 TATCGATATGCCATGTGTGCTAGCCAGAACAGATCACGGCAGATATGCTATTGCA 2760
Db	2701 TATCGATATGCCATGTGTGCTAGCCAGAACAGATCACGGCAGATATGCTATTGCA 2760	QY	2701 TATCGATATGCCATGTGTGCTAGCCAGAACAGATCACGGCAGATATGCTATTGCA 2760
Db	2761 CTTGACGCAAATATGGAAGGTAAGTGTGTTGCTAGGATTCAGGATTTCACTCACGTTTCGATAAA 180	QY	2761 CTTGACGCAAATATGGAAGGTAAGTGTGTTGCTAGGATTCAGGATTTCACTCACGTTTCGATAAA 180
Db	2761 CTTGACGCAAATATGGAAGGTAAGTGTGTTGCTAGGATTCAGGATTTCACTCACGTTTCGATAAA 180	QY	2761 CTTGACGCAAATATGGAAGGTAAGTGTGTTGCTAGGATTCAGGATTTCACTCACGTTTCGATAAA 180
Db	2821 GCGGCCAACAGGAAACAGAAATCCCCAACGCTAACCGCTGGCTTCGACGGATTGAA 2880	QY	2821 GCGGCCAACAGGAAACAGAAATCCCCAACGCTAACCGCTGGCTTCGACGGATTGAA 2880
Db	2821 GCGGCCAACAGGAAACAGAAATCCCCAACGCTAACCGCTGGCTTCGACGGATTGAA 2880	QY	2821 GCGGCCAACAGGAAACAGAAATCCCCAACGCTAACCGCTGGCTTCGACGGATTGAA 2880
Db	2881 GGTCACTCCGTTGGAATGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 2880	QY	2881 GGTCACTCCGTTGGAATGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 2880
Db	2881 GGTCACTCCGTTGGAATGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 2880	QY	2881 GGTCACTCCGTTGGAATGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 2880
Db	2941 GGCATAATAAGTTCTTAAGGTGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 2940	QY	2941 GGCATAATAAGTTCTTAAGGTGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 2940
Db	2941 GGCATAATAAGTTCTTAAGGTGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 2940	QY	2941 GGCATAATAAGTTCTTAAGGTGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 2940
Db	3001 TTCTGTGTTAGTAGGTGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 3060	QY	3001 TTCTGTGTTAGTAGGTGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 3060
Db	3001 TTCTGTGTTAGTAGGTGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 3060	QY	3001 TTCTGTGTTAGTAGGTGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 3060
Db	3061 GATGGGTTTATGATTAGGTGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 3120	QY	3061 GATGGGTTTATGATTAGGTGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 3120
Db	3061 GATGGGTTTATGATTAGGTGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 3120	QY	3061 GATGGGTTTATGATTAGGTGTTACGGCTAACCGCTGGCTTCGACGGATTGAA 3120
Db	3121 TATGGCGCGCAACTGGGATAATTATCGCGCGGGTGTACATCTATGTACTAGATCGAA 3180	QY	3121 TATGGCGCGCAACTGGGATAATTATCGCGCGGGTGTACATCTATGTACTAGATCGAA 3180

Db	601	GAGACGAGGAAGAAGATTGGGTCAAGTTAACAAACAGAGACACTCGTATTAGTTGGA	660	QY	1741	TTTAATTAATAAAGGAATATATTATGCAAACATCATCACACATATCCA	1800
QY	661	CTTGGTAGCAAGTCGATTATTGCCAGTAACAACTGGTACACAACGACA	720	Db	1741	TTTAATTAATAAAGGAATATATTATGCAAACATCATCACACATATCCA	1800
Db	661	CTTGGTAGCAAGTCGATTATTGCCAGTAACAACTGGTACACAACGACA	720	QY	1801	TGAAATCTCATAGTACACAAGTAGAGAAATAATTAGATACAAACTTCTA	1860
QY	721	TCGTTATTAGTTGACTTGTTACCTRGGTTAGAAAAGTGATAAGTTAAC	780	Db	1801	TGAAATCTCATAGTACACAAGTAGAGAAATAATTAGATACAAACTTCTA	1860
Db	721	TCGTTATTAGTTGACTTGTTACCTRGGTTAGAAAAGTGATAAGTTAAC	780	QY	781	TGTTCATAGGGTGATTGTTAGGAACTTGGTTAGAAAGTTGACTAGGG	840
QY	781	TGTTCATAGGGTGATTGTTAGGAACTTGGTTAGAAAGTTGACTAGGG	840	Db	781	TGTTCATAGGGTGATTGTTAGGAACTTGGTTAGAAAGTTGACTAGGG	840
Db	841	TACAAAGTTAGATTAGTTAACATTTGACAGGTTAACATTAAACATT	900	QY	841	TACAAAGTTAGATTAGTTAACATTTGACAGGTTAACATTAAACATT	900
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QY	901	TTACACCGATTTCCCTGACAGAAATTCTACAGTTAACATTAAAC	960	QY	901	TTACACCGATTTCCCTGACAGAAATTCTACAGTTAACATTAAAC	960
Db	901	TTACACCGATTTCCCTGACAGAAATTCTACAGTTAACATTAAAC	960	Db	901	TTACACCGATTTCCCTGACAGAAATTCTACAGTTAACATTAAAC	960
QY	961	GACAATTAACTTAACTAACATTAAACATTAAACACCACAA	1020	QY	961	GACAATTAACTTAACTAACATTAAACACCACAA	1020
Db	961	GACAATTAACTTAACTAACATTAAACACCACAA	1020	Db	961	GACAATTAACTAACATTAAACACCACAA	1020
QY	1021	TATGCTTACTCTCTTGTAGAAACTAACTATACATATAAATCT	1080	QY	1021	TATGCTTACTCTCTTGTAGAAACTAACTATACATATAAATCT	1080
Db	1021	TATGCTTACTCTCTTGTAGAAACTAACTATACATATAAATCT	1080	Db	1021	TATGCTTACTCTCTTGTAGAAACTAACTATACATATAAATCT	1080
QY	1081	AATCATTATTGTAATATGCAATTGCAATTGTAATGACGG	1140	QY	1081	AATCATTATTGTAATATGCAATTGCAATTGTAATGACGG	1140
Db	1081	AATCATTATTGTAATATGCAATTGCAATTGTAATGACGG	1140	Db	1081	AATCATTATTGTAATATGCAATTGCAATTGTAATGACGG	1140
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Db	1141	TTATCACTTGCACCAAAATGATTGGATTAGTCCAAATGCAATT	1200	Db	1141	TTATCACTTGCACCAAAATGATTGGATTAGTCCAAATGCAATT	1200
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Db	1201	CTCTGTGCTTAATGATTCTCAATTTCTTAACTACAGAGCTACA	1260	Db	1201	CTCTGTGCTTAATGATTCTCAATTTCTTAACTACAGAGCTACA	1260
QY	1261	TTTATATTGTAATCTAAATGACAGGGAAACTTCATAGAGATT	1320	QY	1261	TTTATATTGTAATCTAAATGACAGGGAAACTTCATAGAGATT	1320
Db	1261	TTTATATTGTAATCTAAATGACAGGGAAACTTCATAGAGATT	1320	Db	1261	TTTATATTGTAATCTAAATGACAGGGAAACTTCATAGAGATT	1320
QY	1321	GGGAACACATCATGAAACGAAACTTTAGCAATCATATCGATT	1380	QY	1321	GGGAACACATCATGAAACGAAACTTTAGCAATCATATCGATT	1380
Db	1321	GGGAACACATCATGAAACGAAACTTTAGCAATCATATCGATT	1380	Db	1321	GGGAACACATCATGAAACGAAACTTTAGCAATCATATCGATT	1380
QY	1381	ACTTAGCGTAACTGAAACTTTCTCTTGTGAACTGTTAATT	1440	QY	1381	ACTTAGCGTAACTGAAACTTTCTCTTGTGAACTGTTAATT	1440
Db	1381	ACTTAGCGTAACTGAAACTTTCTCTTGTGAACTGTTAATT	1440	Db	1381	ACTTAGCGTAACTGAAACTTTCTCTTGTGAACTGTTAATT	1440
QY	1441	TTGTCGAATCTTTCTCTTGTGAACTGTTAATT	1500	QY	1441	TTGTCGAATCTTTCTCTTGTGAACTGTTAATT	1500
Db	1441	TTGTCGAATCTTTCTCTTGTGAACTGTTAATT	1500	Db	1441	TTGTCGAATCTTTCTCTTGTGAACTGTTAATT	1500
QY	1501	TGTGAACTTGTGAACTTGTGAACTTGTGAACTTGTGAACT	1560	QY	1501	TGTGAACTTGTGAACTTGTGAACTTGTGAACTTGTGAACT	1560
Db	1501	TGTGAACTTGTGAACTTGTGAACTTGTGAACTTGTGAACT	1560	Db	1501	TGTGAACTTGTGAACTTGTGAACTTGTGAACTTGTGAACT	1560
QY	1561	TCCCTGTTATGTGATAGCTTGTTACTTGCAATTGTTAATT	1620	QY	1561	TCCCTGTTATGTGATAGCTTGCAATTGTTAATT	1620
Db	1561	TCCCTGTTATGTGATAGCTTGCAATTGTTAATT	1620	Db	1561	TCCCTGTTATGTGATAGCTTGCAATTGTTAATT	1620
QY	1621	AAATAACATGTAACGAACTTGTGAACTTGTGAACTTGTGAACT	1680	QY	1621	AAATAACATGTAACGAACTTGTGAACTTGTGAACTTGTGAACT	1680
Db	1621	AAATAACATGTAACGAACTTGTGAACTTGTGAACTTGTGAACT	1680	Db	1621	AAATAACATGTAACGAACTTGTGAACTTGTGAACTTGTGAACT	1680
QY	1681	TACTCATGATAGTTTTTTGAAATGCTTAATTAATGCTTCTAAT	1740	QY	1681	TACTCATGATAGTTTTTTGAAATGCTTAATTAATGCTTCTAAT	1740
Db	1681	TACTCATGATAGTTTTTTGAAATGCTTAATTAATGCTTCTAAT	1740	Db	1681	TACTCATGATAGTTTTTTGAAATGCTTCTAATTAATGCTTCTAAT	1740
QY	2760	CTGACGCAATATGGAAGGTTAGTTGATAATGGGATCGCTCAGG	2819	QY	2760	CTGACGCAATATGGAAGGTTAGTTGATAATGGGATCGCTCAGG	2819

QY 2821 GCGGCCAACAGGAACAGAAATTCCCCAAGTTAACGAGCCGTTGCAGGGATTGAA 2880 /translation="MALKHMOIIFLFVAIFISSFCFSITLSRPLDNEIMQKRHEWMTK  
Db 2820 GCGGCCAACAGGAACAGAAATTCCCCAAGTTAACGAGCCGTTGCAGGGATTGAA 2879 HGRVYADVKEENRYVVEKNVERIEHNSIPAGRTEFLAVNQFADLTNDFCSMYTG  
QY 2881 GGTCACTCCGTTCCAATGTTAGGTACGCCAGCCCTGAGCTCGATCGTCAAACATT 2940 FKGVSAISQSOTKMSPFYONVSSGALPVSDWRRKGAVPTKNOGSCGCCWAFAV  
Db 2880 GGTCACTCCGTTCCAATGTTAGGTACGCCAGCCCTGAGCTCGATCGTCAAACATT 2939 AIEGATOIKKGKLISLSQLVDCDTNDFGCEGLMDTAFFHKATGGLTESDYP  
QY 2941 GGCAATAAAGTTCTTAAGATTGAAATCCTGTTGCCGTTGCGGATGATTATAAT 3000 KGEDATCNSKKTNPKATSITGYEDVPVNEQALMKAVAHQPVSVGIEGGDFQFYSS  
Db 2940 GGCATAAAGTTCTTAAGATTGAAATCCTGTTGCCGTTGCGGATGATTATAAT 2999 GVFTGECTYLDDHAWTAIGYESTNGSKYWIKNNGTNGESGYMRIQKDVKDKQQL  
QY ORIGIN  
Db 3001 TTCTGTGAATTACGTTAACATGTAATAATTAACATGTAATGCACTGACGTTTATGA 3060 ORIGIN  
QY 3061 GATGGGTTTATGATTAGTAGTCGGATAATAACATGTAATGCACTGACGTTTATGA 3059 Query Match 68.6%; Score 2182.4; DB 8; Length 3659;  
Db 3060 GATGGGTTTATGATTAGTAGTCGGATAATAACATGTAATGCACTGACGTTTATGA 3120 Best Local Similarity 100.0%; Pred. No. 0;  
QY Db 3121 TATGGCGCGCAAACGGATAAATTACGGATAATAACATGTAATGCACTGACGTTTATGA 3119 Matches 2183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 3120 TATGGCGCGCAAACGGATAAATTACGGATAATAACATGTAATGCACTGACGTTTATGA 3180 QY 61 CTCGTGGAGCACCGACTCTGTTTATAGAAACCCGATTGTTAGACTGAGAC 120  
QY Db 3181 TTC 3183 121 AAAAAGTAATCGTGATTAAATTAAATTAGTTCATCACGTTGAGAC 120  
Db 3180 TTC 3182 121 AAAAAGTAATCGTGATTAAATTAAATTAGTTCATCACGTTGAGAC 180  
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LOCUS ATU37336  
DEFINITION Arabidopsis thaliana senescence-specific protein (SAG12) gene,  
ACCESSION U37336  
VERSION U37336 . 1 GI:1046372  
KEYWORDS ·  
SOURCE ·  
ORGANISM Arabidopsis thaliana (thale cress)  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicots; rosids; eurosids II; Brassicales; Brassicaceae; core eudicots;  
1 (bases 1 to 3659)  
AUTHORS Gan,S. and Amasino,R.M.  
TITLE Inhibition of leaf senescence by autoregulated production of  
cytokinin  
JOURNAL Science 270 (5244), 1986-1988 (1995)  
REFERENCE 2 (bases 1 to 3659)  
AUTHORS Gan,S.  
TITLE Direct Submission  
JOURNAL Submitted (30-SEP-1995) Susheng Gan, Biochemistry, University of  
Wisconsin-Madison, 420 Henry Mall, Madison, WI 53706, USA  
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Db 8592746 /organism="Arabidopsis thaliana"  
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 VKTIDEEKMTKVKSSLQEDAADIPIATVAYEMENEVGEPNVVDQALDKQBEAMARLL  
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 AGGEERGK"  
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CDS

Query	Match	Score	DB	Length
Best Local Similarity	65.2%	2075.8	DB 8	Length 59648;
Matches 2166; Conservative	98.8%	Pred. No. 0;	Mismatches 0;	Indels 10; Gaps 7;
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61	CTCGTGGAGCACCGAGTCTGTTTATATTAGAACCCGATGTGATTTAGACTGAGAC	120	Db	29516 ATAATTCTAATCATTATTTGTAATATGCAGTTATGGTCAATTGGATTAGTAT
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121	AAAAAAGTAAATCGTTGATGTTAAATTAAATTAGAACCCGATGTGATTTAGACTGAGAC	180	Db	29576 TTAGAC-GTTATCACTTCAGCCAAATATGATTGGTTAAGTCCAAATGCAATTTCG
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654	GTGTTGACTTTGGTAGCAAGTCGATTATTGCCAGTAACACTGACA	713	Qy	1672 AATAATTACTCATGATAGATTTTTGTAATGTCATTAAATGCTTCT
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714	ACTCGTATCGTTATTAGTTGACTTGGTACCTTGGT-AAGAAAAGTGTATAGT	772	Qy	1732 AATAATTACTCATGATAGATTTTTGTAATGTCATTAAATGCTTCT
29156	ACTCGTATCGTTATTAGTTGACTTGGTACCTTGGTCAAGTCAAGAAAAGTGTATAGT	29215	Db	30175 AATAATTACTCATGATAGATTTTTGTAATGTCATTAAATGCTTCT
773	AAATCAGTTGTCTCATGAGGTGATTGTTAATTGTCAGTTGACTAGGGCGATTCTTCA	832	Qy	1792 TATCCAACCTCGAAATCTCTATAGTACACAGTAACACTGACA
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833	CATCACACATAACAAAGTTTATAGA-TTTTTTATAACATTTGCCACGGCTCGTA	891	Qy	1852 AACTTCCTAATCATCAATTAAAGTTACAAACTAATTAAACCCACCACTAAATT
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892	AGTTGGTATTACACCGCATTTCCCTGTACAGAAATTCACTATATTATTAT	951	Qy	1912 ACTAAACATCCGAGCAAGTGAACAGACTTGATTCACTTGAGTTGAGACTAA
29336	AGTTGGTATTACACCGCATTTCCCTGTACAGAAATTCACTATATTATTAT	29395	Db	30355 ACTAAACATCCGAGCAAGTGAACAGACTTGATTCACTTGAGTTGAGACTAA
952	ACTCCAGTTGACATTATAAGTTAACGTTTACATTAAATTACATGTGAG	1011	Qy	1972 ATGGCTACGTATCAACACATCAACGATCATTAGTATGATGATGTTAGTCATTAC
29396	ACTCCAGTTGACATTATAAGTTAACGTTTACATTAAATTACATGTGAG	29455	Db	30415 ATGGCTACGTATCAACACATCAACGATCATTAGTATGATGATGTTAGTCATTAC
1012	ATCCAAGAATATGCTACTCTCTTGTGTAAGAAACTAATCACTATAATAA	1071	Qy	2092 TCAACTTATTCACTATAACCCATCTCAGTACCCCTCTGAAGTAATCAATAAG

Db 30535 TCAACCTTCACTATAAACCCATCTCAGTACCCCTCTGAAGTAATCAAATTAG 30594  
Qy 2152 AGCAAAGTCATTAACCTTCCTAAACCATTGG 2184  
Db 30595 AGCAAAAGTCATTTACTTCCTAAACAATGG 30627

RESULT 5

TIPMR TIPMR 1296 bp DNA linear BCT 13-MAR-1996  
LOCUS Ti plasmid (from *A.tumefaciens* octopine strain) tumor morphology  
DEFINITION Ti plasmid (from *A.tumefaciens* octopine strain) tumor morphology  
ACCESSION K02000  
VERSION K02000.1 GI:154744  
KEYWORDS tmr gene; tumor morphology gene.  
SOURCE Plasmid Ti  
ORGANISM Plasmid Ti  
plasmids.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Lichtenstein,C., Klee,H., Montoya,A., Garfinkel,D., Fuller,S.,  
Flores,C., Nester,E. and Gordon,M.  
TITLE Nucleotide sequence and transcript mapping of the tmr gene of the  
*ptIA6NC* octopine Ti-plasmid: a bacterial gene involved in plant  
tumorigenesis  
JOURNAL J. Mol. Appl. Genet. 2 (4), 354-362 (1984)  
MEDLINE 84241512  
PUBMED 6330262

COMMENT Original source text: Plasmid Ti (clone: *ptIA6NC*) DNA.  
The T-DNA of *ptIA6NC* encodes eight polyadenylated transcripts (see  
sites table), and includes at least four genes: tmr - tmr - tmr - tmr.

FEATURES Location/Qualifiers

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ORIGIN 505 bp upstream of BamHI site.

Query Match 23.0%; Score 733.4; DB 1; Length 1296;  
Best Local Similarity 96.0%; Pred. No. 3.1e-106;  
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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Db 2199 TTTCGGTCCAACTTGCACAGGAAGACGACGGCATAGCTCTTGCCAGCAGACGG 2258  
Qy 2259 GCTTCGAGTCCTTCGCTGATCGGTCAATCGTCCTCAACTATCACCGAAGCG 2318  
Db 231 TTTCGGTCCAACTTGCACAGGAAGACGACGGCATAGCTCTTGCCAGCAGACGG 290

Qy 2319 ACGACCAACAGTGGAAACTGAAGAACGACGGCATCTACTTGATGATCGGCCT 2378  
Db 351 ACGACCAACAGTGGAAACTGAAGAACGACGGCATCTACTTGATGATCGGCCT 410

Qy 2379 GGTTGGAGGTATCATCGCAGCAGAACGCTCATCAGGTATCGAGGGTATAA 2438  
Db 411 GGTGGAGGTATCATCGCAGCAGAACGCTCATCAGGTGTATCGAGGGTATAA 470

Qy 2439 TCATGAGGCCAACGGCGGGCTTATCTGGAGGATCCACCTCGTTGCTCAACTGCA 2498  
Db 471 TCATGAGGCCAACGGCGGGCTTATCTGGAGGATCCACCTCGTTGCTCAACTGCA 530

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Qy 2919 GAG 2921  
Db 951 GCG 953

RESULT 6

ATTMR ATTMR 1988 bp DNA linear BCT 12-SEP-1993  
LOCUS Agrobacterium tumefaciens tmr-gene encoded by the octopine Ti  
DEFINITION Agrobacterium tumefaciens tmr-gene encoded by the octopine Ti  
plasmid (tumor inducing).

ACCESSION X00010  
VERSION X00010.1 GI:39172  
KEYWORDS octopine synthetase; plasmid.  
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)  
ORGANISM Agrobacterium tumefaciens  
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

REFERENCE 1 (bases 1 to 1988)  
 AUTHORS Heidekamp, F., Dirkse, W.G., Hille, J. and van Ormondt, H.  
 TITLE Nucleotide sequence of the Agrobacterium tumefaciens octopine Ti plasmid-encoded tmr gene  
 JOURNAL Nucleic Acids Res. 11 (18), 6211-6223 (1983)  
 MEDLINE 84015366  
 PUBMED 6312414  
 COMMENT The product of the tmr-gene inhibits root formation of the tumors on certain plant species and appears to play a role in the cytokinin-independent growth of transformed cells.  
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 Best Local Similarity 96.0%; Pred. No. 2.9e-106;  
 Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
 QY 2139 TAATCAAATTAGAGCAAAAGTCATTAACTTCTAAACCATGGACCCCTGCATCTAA 2198  
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 Db 767 GCTTCAGTCTTCGCTTGTATCGGGTCCAATGCTGTCTCAACTATAACCGGAGGG 826  
 QY 2319 ACGACCAACAGTGAAGAACTGAAAGGAAACGACGCCGCTCTACCTGTATGATCGGCCTCT 2378  
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REFERENCE 2619 TGCAGGCCATTTCAGAGTTATCTTGGAACTCGGCTGAGGCC 2678  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE 4 (bases 1 to 24595)  
 AUTHORS Guevara-Garcia, A., Mosqueda-Cano, G., Arguello-Astorga, G., Simpson, J. and Herrera-Estrella, L.  
 TITLE Tissue-specific and wound-inducible pattern of expression of the mannopine synthase promoter is determined by the interaction between positive and negative cis-regulatory elements  
 JOURNAL Plant J. 4 (3), 495-505 (1993)  
 MEDLINE 94035196  
 PUBMED 8220492  
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		DEFINITION	Ti plasmid T-DNA region.
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		VERSION	E00404.1
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Query	Match	Score	23.0%; Score 733.4;
	Best Local Similarity	DB	1; DB 1;
	Matches	Pred. No.	96.0%; 2.1e-106;
	752; Conservative	Mismatches	0; Mismatches 31;
		Indels	0; Indels 0;
		Gaps	Gaps 0;
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QY	2379 GGTGGAGGGTATCATCGCAGCCAAGCAAGCTCATCATAGGCTGATCGAGGGGTATAA	2438	
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QY	2439 TCATGAGGCCAACGGGGGCTTATTCTGAGGGAGGATCCACCTCGTGTCTCAACTGCT	2498	
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LOCUS	E00404	linear	PAT 29-SEP-1997

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DEFINITION			PAT	29-SEP-1997
ACCESSION	E00546			
VERSION	E00546.1			
KEYWORDS	JP 1985256383-A/1.			
SOURCE	Agrobacterium tumefaciens (Rhizobium radiobacter)			
ORGANISM				
REFERENCE				
AUTHORS	Richiyaado, E.B. and Jiyon, D.K.			
TITLE	PROMOTOR OF OCTOPINE T-DNA			
JOURNAL	Patent: JP 1985256383-A 1 18-DEC-1985;			
COMMENT	AGURIJIENEIKUSU RES ASSOC LTD			
OS	Agrobacterium tumefaciens			
PN	JP 1985256383-A/1			
PD	18-DEC-1985			
PF	19-NOV-1984 JP 1984244307			
PR	18-NOV-1983 US 83 553786			
PI	RICHIYAADO EFU BEKKA, JIYON DEI KENPU			
PC	C12N15/00, A01H1/00, C12N1/20, C12N5/00//C07H21/04, (C12N1/20, PC			
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CC	topology: Linear;			
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CC	anti-sense: No;			
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DEFINITION	Octopine T-DNA promoters					Db	9508 GCG 9510
ACCESSION	AR364803						
VERSION	AR364803.1						
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 24595)						
AUTHORS	Barker,R.F. and Kemp,J.D.						
TITLE	Octopine T-DNA promoters						
JOURNAL	Patent: US 5428147-A 1 27-JUN-1995;						
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ORIGIN							
Query Match	23.0%; Score 733.4; DB 6; Length 24595;						
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Db	9328 CACGGCAGATATGCTATGCCAGGATATGGCAAGTAACTGGAT 2798					QY	2139 TAATCAAATTAAGGCAAAAGTCATTAACCTTCTAAACCATGGACCCCTGCATCTAAT 2798
Db	9328 CACGGCAGATATGCTATGCCAGGATATGGCAAGTAACTGGAT 9387					QY	2139 TAATCAAATTAAGGCAAAAGTCATTAACCTTCTAAACCATGGACCCCTGCATCTAAT 9387
Db	9389 CGCTCAGGAGTATTCTCATGCCAACAGGAACAGAAATCCCCAAGTAACTGC 2858					QY	2139 TAATCAAATTAAGGCAAAAGTCATTAACCTTCTAAACCATGGACCCCTGCATCTAAT 2858
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QY	2859 AGCCGCTTCGACGGATTCAAAGGTCACTCGTCAAGTATTAGTTACGCCAGCCCT 2918					QY	2139 GGCGCGAACAGCTATTGGAGTGCAGATTCTGTTGGCATATTATGCCACAAGTAC 2558

		REFERENCE	5 (bases 50125 to 54471)
		AUTHORS	Habeeb,L.F., Wang,L. and Winans,S.C.
		TITLE	Transcription of the octopine catabolism operon of the Agrobacterium tumor-inducing plasmid pTiA6 is activated by a LysR-type regulatory protein
Db	9088 GGCAGAACAGCTATTGGACTGCAGATTCGATATTGCCACAAGTAC 9147	JOURNAL	Mol. Plant Microbe Interact. 4 (4), 379-385 (1991)
QY	2559 CGACCAAAGAGACTTCATGAAGCCAAAGCCAGTTAACAGATGGCACCCG 2618	PUBMED	92190631
Db	9148 CGACCAAAGAGACTTCATGAAGCCAAAGCCAGTTAACAGATGGCACCCG 9207	REFERENCE	1799699
QY	2619 TGCAGGCCATTCTTATTCAAGAGTTACAGGTGGTTATCTTGAAATGAACTTCGGCTGAGGCC 2678	AUTHORS	6 (bases 50125 to 54471)
Db	9208 TGCAGGCCATTCTTATTCAAGAGTTACAGGTGGTTATCTTGAAATGAACTTCGGCTGAGGCC 9267	TITLE	Valdivia,R.H., Wang,L. and Winans,S.C.
QY	2679 CATTCTGAAAGAGATCGATGGATATCGATATGCCATGCTGGTTATCTTGAAATGAACTTCGGCTGAGGCC 2738	JOURNAL	Characterization of a putative periplasmic transport system for octopine accumulation encoded by Agrobacterium tumefaciens Ti plasmid pTiA6
Db	9268 CATTCTGAAAGAGATCGATGGATATGCCATGCTGGTTATCTTGAAATGAACTTCGGCTGAGGCC 9327	PUBMED	J. Bacteriol. 173 (20), 6398-6405 (1991)
QY	2739 CACGGCAGATATGCTATTGAGCTTGAGCTTGAGCAATATGAAAGCTTAAGTTAGGT 2798	REFERENCE	92011411
Db	9328 CACGGCAGATATGCTATTGAGCTTGAGCTTGAGCAATATGAAAGCTTAAGTTAGGT 9327	AUTHORS	1655707
QY	9388 CGCTCAGGAGTATTTCATCATGGGCCAACAGAACAGAAATTCCCCAACAGAACAGAAATTCCCCAACAGAACAG 9447	TITLE	Kim,K.S. and Farrand,S.K.
Db	9448 AGCCGCTTTCGAGGATTGGATTCATCGGCTTGGAAATGTTACGCCAGCC 9507	REFERENCE	Ti-Plasmid-encoded genes responsible for catabolism of the crown gall opine mannopine by Agrobacterium tumefaciens are homologs of the T-region genes responsible for synthesis of this opine by the plant tumor
QY	2859 AGCCGCTTTCGAGGATTGGATTCATCGGCTTGGAAATGTTACGCC 2858	AUTHORS	J. Bacteriol. 178 (11), 3275-3284 (1996)
Db	9448 AGCCGCTTTCGAGGATTGGATTCATCGGCTTGGAAATGTTACGCCAGCC 9507	TITLE	8 (bases 39167 to 45466)
QY	2919 GAG 2921	REFERENCE	Fuqua,C. and Winans,S.C.
Db	9508 GCG 9510	AUTHORS	Localization of OCCR-activated and trar-activated promoters that express two ABC-type permeases and the trar gene of Ti plasmid pTiR10
RESULT 12			
LOCUS	AF242881	JOURNAL	Mol. Microbiol. 20 (6), 1199-1210 (1996)
DEFINITION	Agrobacterium tumefaciens octopine-type Ti plasmid, complete sequence.	MEDLINE	96405643
ACCESSION	AF242881 AF034854 AF034855 AF035413 AF035773 AF039887 AF039888 U48718 U60011 X04784 AF242881.1 GI:8572673	REFERENCE	8809772
VERSION	.	AUTHORS	Alt-Morbe,J., Stryker,J.L., Fuqua,C., Li,P.L., Farrand,S.K. and Winans,S.C.
KEYWORDS	Agrobacterium tumefaciens (Rhizobium radiobacter)	TITLE	The conjugal transfer system of Agrobacterium tumefaciens Octopine-type Ti plasmids is closely related to the transfer system of an IncP plasmid and distantly related to Ti plasmid vir genes J. Bacteriol. 178 (14), 4248-4257 (1996)
SOURCE	Agrobacterium tumefaciens	JOURNAL	95312368
ORGANISM	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.	MEDLINE	8763954
REFERENCE	1 (bases 193234 to 194140; 1 to 23692)	REFERENCE	10 (bases 54312 to 62806)
AUTHORS	Barker,R.F., Idler,K.B., Thompson,D.V. and Kemp,J.D.	AUTHORS	Oger,P., Kim,K.S., Sackett,R.L., Piper,K.R. and Farrand,S.K.
TITLE	Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octopine Ti plasmid PTi15955	TITLE	Octopine-type Ti plasmids code for a mannopine-inducible dominant-negative allele of traR, the quorum-sensing activator that regulates Ti-Plasmid conjugal transfer
JOURNAL	Plant Mol. Biol. 2, 335-350 (1983)	JOURNAL	Mol. Microbiol. 27 (2), 277-288 (1998)
REMARK	original sequence presented in GenBank Accession Number X00493	MEDLINE	98143415
REFERENCE	2 (bases 166443 to 168193)	PUBMED	9484884
AUTHORS	Yanofsky,M.F. and Nester,E.W.	REFERENCE	11 (bases 133963 to 138972)
TITLE	Molecular characterization of a host-range-determining locus from Agrobacterium tumefaciens	AUTHORS	Kalogeraki,V.S. and Winans,S.C.
JOURNAL	J. Bacteriol. 168 (1), 244-250 (1986)	TITLE	Wound-released chemical signals may elicit multiple responses from an Agrobacterium tumefaciens strain containing an octopine-type Ti plasmid
MEDLINE	87008387	JOURNAL	J. Bacteriol. 180 (21), 5660-5667 (1998)
PUBMED	3759904	MEDLINE	99009000
REFERENCE	3 (bases 168089 to 173951)	PUBMED	9791116
AUTHORS	Yanofsky,M.F., Porter,S.G., Young,C., Albright,L.M., Gordon,M.P. and Nester,E.W.	REFERENCE	12 (bases 76455 to 98723)
TITLE	The virD operon of Agrobacterium tumefaciens encodes a site-specific endonuclease	AUTHORS	Lyi,S.M., Jafri,S. and Winans,S.C.
JOURNAL	Cell 47 (3), 471-477 (1986)	TITLE	Mannopinic acid and agropinic acid catabolism region of the Octopine-type Ti plasmid PTi15955
MEDLINE	87028239	JOURNAL	Mol. Microbiol. 31 (1), 339-347 (1999)
PUBMED	3021341	MEDLINE	9987134
REFERENCE	4 (bases 175278 to 177719)	PUBMED	13 (bases 1 to 194140)
AUTHORS	Winans,S.C., Allenza,P., Stachel,S.E., McBride,K.E. and Nester,E.W.	REFERENCE	Winans,S.C., Zhu,J., Oger,P.M., Schrammeijer,B., Hooykaas,P.J. and Farrand,S.K.
TITLE	Characterization of the virE operon of the Agrobacterium Ti plasmid pTiA6	AUTHORS	Octopine-type Ti plasmid sequence
JOURNAL	Nucleic Acids Res. 15 (2), 825-837 (1987)	TITLE	Unpublished
MEDLINE	87146396	REFERENCE	14 (bases 68024 to 76460)
PUBMED	3547330	AUTHORS	Kim,K.-S.
TITLE			

JOURNAL	Submitted (10-JAN-1995) Kun-Soo Kim, Microbiology, University of Illinois at Urbana-Champaign, 1201 W. Gregory Dr., Urbana, IL 61801, USA	source	octopine-type" 13244. 1.13618 /organism="Agrobacterium tumefaciens"
REFERENCE	15 (bases 96353 to 111409)		/mol_type="genomic DNA"
AUTHORS	Winans,S.C.		/db_xref="taxon:358"
TITLE	Direct Submission		/insertion_seq="ybd"
JOURNAL	Submitted (20-DEC-1995) Stephen C. Winans, Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA	source	13636. .14181
REFERENCE	16 (bases 39167 to 45466)		/organism="Agrobacterium tumefaciens"
AUTHORS	Fugua,C.		/mol_type="genomic DNA"
TITLE	Direct Submission		/db_xref="taxon:358"
JOURNAL	Submitted (07-FEB-1996) Clay Fuqua, Biology, Trinity University, 715 Stadium Dr., San Antonio, TX 78212, USA	source	/insertion_seq="ybe"
REFERENCE	17 (bases 54312 to 62806)		/note="similar to IS66"
AUTHORS	Kim,K.-S., Sackett,R.L. and Farrand,S.K.		14183. .14666
TITLE	Direct Submission		/organism="Agrobacterium tumefaciens"
JOURNAL	Submitted (04-JUN-1996) Crop Sciences, University of Illinois at Urbana-Champaign, 240 ERML, 1201 W. Gregory Dr., Urbana, IL 61801, USA	source	18 (bases 186239 to 193239)
REFERENCE	Zhu,J. and Winans,S.C.		Zhu,J. and Winans,S.C.
AUTHORS	Direct Submission		Best Local Similarity 96.0%; Pred. No. 1.6e-106; Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
TITLE	Submitted (17-NOV-1997) Section of Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA	Query	2139 TAATCAAATTAGGCAAAAGTCATTACTTCTAAACATGGACCCCTGCATCTAAT 2198
JOURNAL	19 (bases 76455 to 98723)	Db	7821 TAATATAAAATCAGTTGTATTCAATATACTGCAAAACTATGGACCATGCTATCTAAT 7880
REFERENCE	Winans,S.C. and Lyi,S.	Qy	2199 TTTCGGTCAACTTGACAGAAGACGACGCCGATAGCTCTGGCCACCGACAGG 2258
AUTHORS	Direct Submission	Db	7881 TTTCGGTCAAATTGCACAGAAAAGACGACGCCGATAGCTCTGGCCAGCAGG 7940
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JOURNAL	20 (bases 170209 to 175283)	Db	7941 GCTTCCAGTCTTCGCTTGATCGGTCAACTATCAACCGGAAGGG 8060
REFERENCE	Zhu,J. and Winans,S.C.	Qy	2319 ACGACCACAGTGAAGAACGACGCCGCTCTACCTTGATGATCGGCCTCT 2378
AUTHORS	Direct Submission	Db	8001 ACGACCACAGTGAAGAACGACGCCGCTCTACCTTGATGATCGGCCTCT 8060
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JOURNAL	21 (bases 133963 to 138972; 176911 to 186244)	Db	8061 GGTGGAGGTATCATCGCAGCCAAGCAAGCTCATCATAGGCTATCGGAGGTATAA 8120
REFERENCE	Styker,J.L., Mantis,N.J., Kalogeraki,V.S. and Winans,S.C.	Qy	8121 TCATGAGGCCAACGGGGCTTATCTGAGGGAGATCCACTCTCGTGTGCTCAACTGCAT 8180
AUTHORS	Direct Submission	Db	2439 TCATGAGGCCAACGGGGCTTATCTGAGGGAGATCCACTCTCGTGTGCTCAACTGCAT 2498
TITLE	Submitted (23-DEC-1997) Microbiology, Cornell University, Ithaca, NY 14853, USA	Qy	8181 GGCAGGAAACAGCTATTGGAGGTGCAAGATTTCTGGCATATTATTCGAGGAGATCCACTCTCGTGTGCTCAACTGCAT 8240
JOURNAL	22 (bases 22855 to 39243)	Db	8241 CGACCAAGAGCTTCATGAAAGGGCAAGGCCAGAGTATCGAGATGGTGCACCCGC 8300
REFERENCE	Winans,S.C.	Qy	2559 CGACCAAGAGCTTCATGAAAGGGCAAGGCCAGAGTATCGAGATGGTGCACCCGC 2618
AUTHORS	Direct Submission	Db	8301 TGCAGGCCATTCTTCATGAAAGGGCAAGGCCAGAGTATCGAGATGGTGCACCCGC 8360
TITLE	Submitted (29-DEC-1998) Crop Sciences, Cornell University, Wing Hall, Ithaca, NY 14853, USA	Qy	8360 TGCAGGCCATTCTTCATGAAAGGGCAAGGCCAGAGTATCGAGATGGTGCACCCGC 8300
JOURNAL	23 (bases 62801 to 66985)	Db	8360 TGCAGGCCATTCTTCATGAAAGGGCAAGGCCAGAGTATCGAGATGGTGCACCCGC 8300
REFERENCE	Oger,P.M.	Qy	2679 CATTCTGAAAGAGATCGATGGATATCGATATGCCATGTTGCTAGGCCAGAGT 2738
AUTHORS	Direct Submission	Db	8361 CATTCTGAAAGAGATCGATGGATATGCCATGTTGCTAGGCCAGAGT 2738
TITLE	Submitted (29-AUG-1999) Section of Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA	Qy	2739 CACGGCAGATATGCTATGAGCTTGAGGTTATCTTGAAATGGAACCTCGGCTGAGGCC 2798
JOURNAL	24 (bases 110822 to 133968)	Db	8421 CACGGCAGATATGCTATGAGCTTGAGGTTATCTTGAAATGGAACCTCGGCTGAGGCC 2798
REFERENCE	Zhu,J. and Winans,S.C.	Qy	8420 CACGGCAGATATGCTATGAGCTTGAGGTTATCTTGAAATGGAACCTCGGCTGAGGCC 2798
AUTHORS	Direct Submission	Db	8420 CACGGCAGATATGCTATGAGCTTGAGGTTATCTTGAAATGGAACCTCGGCTGAGGCC 2798
TITLE	Submitted (18-AUG-1999) Section of Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA	Qy	8421 CACGGCAGATATGCTATGAGCTTGAGGTTATCTTGAAATGGAACCTCGGCTGAGGCC 2798
JOURNAL	25 (bases 1 to 194140)	Db	8421 CACGGCAGATATGCTATGAGCTTGAGGTTATCTTGAAATGGAACCTCGGCTGAGGCC 2798
REFERENCE	Zhu,J., Oger,P.M., Schrammeijer,B., Hooykaas,P.J., Farrand,S.K. and Winans,S.C.	Qy	8420 CACGGCAGATATGCTATGAGCTTGAGGTTATCTTGAAATGGAACCTCGGCTGAGGCC 2798
AUTHORS	Direct Submission	Db	8420 CACGGCAGATATGCTATGAGCTTGAGGTTATCTTGAAATGGAACCTCGGCTGAGGCC 2798
TITLE	Submitted (07-MAR-2000) Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA	Qy	8420 CACGGCAGATATGCTATGAGCTTGAGGTTATCTTGAAATGGAACCTCGGCTGAGGCC 2798
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		Db	8541 AGCCGCTTCGACGGATCCGAAAGTCATCCGTTGGAATGTTACGCCAGCCCT 8600
		Qy	2919 GAG 2921

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LOCUS	Sequence 2 from patent US 5689042.	LOCUS	Sequence 2 from patent US 6359197.
DEFINITION	709 bp DNA linear	DEFINITION	709 bp DNA linear
ACCESSION	PAT 03-APR-1998	ACCESSION	PAT 20-APR-2002
VERSION	175097	VERSION	AR201517
KEYWORDS	JOURNAL	KEYWORDS	AR201517.1 GI:20252405
SOURCE	Amasino, R.M. and Gan, S.	SOURCE	Unknown.
ORGANISM	Transgenic plants with altered senescence characteristics	ORGANISM	Unknown.
REFERENCE	Patent: US 5689042-A 2 18-NOV-1997;	REFERENCE	Unclassified.
AUTHORS	Location/Qualifiers	AUTHORS	1 (bases 1 to 709)
TITLE	1. .709	TITLE	Amasino, R.M., Gan, S. and Noh, Y.-S.
JOURNAL	/organism="unknown"	JOURNAL	Transgenic plants with altered senescence characteristics
FEATURES	/mol_type="unassigned DNA"	FEATURES	Patent: US 6359197-A 2 19-MAR-2002;
source		source	Location/Qualifiers
ORIGIN		ORIGIN	1 (bases 1 to 709)
Query Match	22.3%; Score 709; DB 6; Length 709;	Query Match	22.3%; Score 709; DB 6; Length 709;
Best Local Similarity	100.0%; Pred. No. 2.4e-102;	Best Local Similarity	100.0%; Pred. No. 2.4e-102;
Matches	709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1532 ATTGATTAGTCAAAGACAAAGAGATCCTGTTATGTGATTAGTGTGATTGTGAT 1591	QY	1532 ATTGATTAGTCAAAGACAAAGAGATCCTGTTATGTGATTAGTGTGATTGTGAT 1591
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QY	1592 GCATGAAAGGTACCTACGTACTACAAGAAAATAACATGTGACTACAGTATCAGCA 1651	QY	1592 GCATGAAAGGTACCTACGTACTACAAGAAAATAACATGTGACTACAGTATCAGCA 1651
Db	121 GCATGAAAGGTACCTACGTACTACAAGAAAATAACATGTGACTACAGTATCAGCA 180	Db	121 GCATGAAAGGTACCTACGTACTACAAGAAAATAACATGTGACTACAGTATCAGCA 180
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 DEFINITION Agrobacterium tumefaciens pTiR37 T-DNA tmr locus.  
 ACCESSION X00639  
 VERSION X00639.1 GI:944822  
 KEYWORDS cytokinin; plasmid.  
 SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)  
 ORGANISM Agrobacterium tumefaciens  
 AUTHORS Goldberg, S.B., Flick, J.S. and Rogers, S.G.  
 TITLE Nucleotide sequence of the tmr locus of Agrobacterium tumefaciens  
 pTi R37 T-DNA  
 JOURNAL Nucleic Acids Res. 12 (11), 4665-4677 (1984)  
 MEDLINE 84247329  
 PUBMED 6330678  
 COMMENT On Aug 15, 1995 this sequence version replaced gi:39174.  
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 QY 2235 GATAGCTCTGCCAGCAGACAGGGCTCCAGCCTTCGCTGTGATCGGGTCCAATCGTG 2294  
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QY 2535 GCATATTTCGCCACAAGTACCCGACCAAGAGACCTCATGAAAGCGGCCAAGGCCAG 2594  
 Db 1012 GCATATTTCGCCACAAGTACCCGACCAAGAGACCTCATGAAAGCGGCCAG 1071  
 QY 2595 AGTTAAGCAGATGTTGCACCCCGCTGCAGGCCATTCTATTCAAGAGTTGGTTATCT 2654  
 Db 1072 AGTTAAGCAGATGTTACGCCCTGCTGCAGGCCATTCTATTCAAGAGTTGGTTATCT 1131  
 QY 2655 TTGGAATGACCTCGGCCATTCTGAAGAGATCGATGGATATCGATATGCAT 2714  
 Db 1132 TTGGAAGAGCCTCGGCCATTCTGAAGAGATCGATGGATATGCATATGCCAT 1191  
 QY 2715 GTTGTGTTGCTAGCCAGAACAGATCACGGCAGATATGCAGCTTGACGCAATAT 2774  
 Db 1192 GTTGTGTTGCTAGCCAGAACAGATCACATCCGATATGCAGCTTGACGCAATAT 1251  
 QY 2775 GGAAGGTAAGTTGATTAATGGATCGCTCAGGATATTGCTATTCATCCATGGCCACAGGA 2834  
 Db 1252 GGAGGATAAGTTGATTCATGGGATCGCTCAGGATATGCAGCTTGACGCAAGA 1311  
 QY 2835 ACAGAAATTCCCCAAGTTAACGCAAGCCGTTTCGACGGATTCAAGGTCATCCGTCAGCCGACAAGA 2894  
 Db 1312 ACAGAAATTCCCTCGAGTTACGCAGCCGTTACGACGGATTCAAGGTCATCCATTGG 1371  
 QY 2895 AATGTTAGGTACGCCAGCCCTGAG 2921  
 Db 1372 AATGTTAGGTACGCCAGCCCTGAG 1398  
 Search completed: June 10, 2004, 05:04:27  
 Job time : 19497 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2004, 18:06:23 ; Search time 1744 seconds  
(without alignments)  
7753.449 Million cell updates/sec

ALIGNMENT

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 9, 2004, 18:06:23 ; Search time 1744 Seconds  
(without alignments)

7753.449 Million cell updates/sec

Title: US-10-072-077A-1

Perfect score: 3183

Sequence: 1 gatatatcttttatattca.....tatgttactagatcgaaatc 3183

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:  
 1: geneseqn1980s:  
 2: geneseqn1990s:  
 3: geneseqn2000s:  
 4: geneseqn2001as:  
 5: geneseqn2001bs:  
 6: geneseqn2002s:  
 7: geneseqn2003as:  
 8: geneseqn2003bs:  
 9: geneseqn2003cs:  
 10: geneseqn2004s:  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	3183	100.0	3183	2	AAT42919	Aat42919 SAG12-1 p
2	3178.2	99.8	3183	6	AAD33601	Aad33601 A. thaliana
3	3171	99.6	3182	6	AAD3336	Aad3336 A. thaliana
4	734.8	23.1	745	2	AAV69757	Isoptenyltransferase gene and NOS terminator.
5	733.4	23.0	1988	6	ABK12492	Agrobacter
6	733.4	23.0	24596	1	AAN50182	Complete
7	730.2	22.9	24593	1	AAN50226	Sequence
8	714.8	22.5	723	3	AAD00619	Agrobacter
9	712.2	22.4	747	3	AAD00624	Agrobacter
10	709	22.3	709	2	AAT42917	SAG12-1 p
11	709	22.3	709	6	AAD33337	Arabidopsis thaliana
12	701.2	22.0	723	1	AAN70790	Sequence
13	569.4	17.9	613	6	AAD44425	Agrobacter
14	536.4	16.9	3017	3	AAC86511	DNA const
15	536	16.8	721	3	AAC86514	Nucleotid
16	536	16.8	723	9	ACF58155	Z. mays i
17	536	16.8	2722	3	AAC86508	DNA const
18	536	16.8	2722	3	AAC86507	DNA compr
19	536	16.8	5622	3	AAC86506	DNA const
20	433.4	13.6	2544	3	AAD00626	Agrobacter
21	344.4	10.8	584	2	AQ78641	Isopentenyltransferase
22	262.8	8.3	7599	4	AAF25320	Nucleotid
23	261.8	8.2	4280	4	AAF25317	Nucleotid

ALIGNMENTS

RESULT 1

AAT42919

ID AAT42919 standard; DNA; 3183 BP.

XX AAT42919;

XX 18-JAN-1997 (first entry)

XX SAG12-1 promoter, isopentenyltransferase gene and NOS terminator.

XX SAG12-1; Promoter; senescence-associated gene; isopentenyltransferase; NOS terminator; Arabidopsis thaliana; development; gene regulation; 5'-untranslated region; cytokinin biosynthesis; transgenic plant; flowering; seed; fruit; crop improvement; ds.

XX OS Arabidopsis thaliana.

XX Key Location/Qualifiers

FH promoter 1. .2073

FT promoter /\*tag= <sup>a</sup> 1473. .2073

FT /\*tag= <sup>b</sup> /note= "Truncated promoter (AAT42917, claim 2)"

FT 5'UTR 2074. .2180

FT /\*tag= <sup>c</sup> 2181. .2920

FT CDS /\*tag= <sup>d</sup> /product= "ISOPENTENYLTRANSFERASE"

FT terminator 2921. .3180

FT /\*tag= <sup>e</sup> /note= "NOS terminator"

FT

XX PN W09629858-A1.

XX PD 03-OCT-1996.

XX PR 20-FEB-1996; 96WO-US002313.

XX PR 29-MAR-1995; 95US-00413135.

XX PA (WISC ) WISCONSIN ALUMNI RES FOUND.

PI Amasino RM, Gan S;

XX DR WPI; 1996-454877/45.

PT Senescence associated gene promoters', SAG12 and SAG13, - useful for  
 PT producing genetic constructs for producing transgenic plants having  
 PT delayed senescence.

XX Example; Page 26-27; 38pp; English.

The sequence represents a full-length version of the SAG12-1 promoter  
 CC (truncated version given in AAT42917) from an *Arabidopsis thaliana*  
 CC senescence-associated gene. The sequence also contains the SAG12-1 gene  
 CC 5'-untranslated region, and has been linked to a cytokinin biosynthesis  
 CC isopentenyltransferase gene and NOS terminator for senescence-specific  
 CC gene expression in a transgenic plant. The resulting transgenic plant  
 CC shows delayed senescence, and shows longer vegetative growth, producing  
 CC more flowers, seeds or fruit

KX Sequence 3183 BP; 1042 A; 527 C; 560 G; 1054 T; 0 U; 0 Other;

Query Match 100.0%; Score 3183; DB 2; Length 3183;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATATCTTTTATTCAAACAAACTAAGTGAGATATGTTGAGAAAGGGACAATT 60  
 1 GATATCTCTTTATTCAAACAAACTAAGTGAGATATGTTGAGAAAGGGACAATT 60

Db 61 CTCTGGAGCACCGAGTCGTGTTATTTAGAAACCGATGTTAGCTAACGTT 120  
 61 CTCTGGAGCACCGAGTCGTGTTATTTAGAAACCGATGTTAGCTAACGTT 120

QY 121 AAAAAGTAATCGTGTGTTAAATTAAATTAGTCTACAGTTTCGATAAA 180  
 121 AAAAAGTAATCGTGTGTTAAATTAAATTAGTCTACAGTTTCGATAAA 180

Db 181 AAATGATTAGTTATCATAGCTAATAGCATGTTCAATTGTTGACACCC 240  
 181 AAATGATTAGTTATCATAGCTAATAGCATGTTCAATTGTTGACACCC 240

QY 241 TTTCCTCTCTTGGTGTCTAACATTAGAGAACCTAACATGTACGTTCAATT 300  
 241 TTTCCTCTCTTGGTGTCTAACATTAGAGAACCTAACATGTACGTTCAATT 300

Db 301 AATAAAACAAATTTCAAGTTTAACTATGTTCAATTTCTAACATGAAACAGTT 360  
 301 AATAAAACAAATTTCAAGTTTAACTATGTTCAATTTCTAACATGAAACAGTT 360

QY 3.61 GAATAGTTGATTATGAATTAGTTAGATCAATACTCAATATGATCAATGTTAT 420  
 3.61 GAATAGTTGATTATGAATTAGTTAGATCAATACTCAATATGATCAATGTTAT 420

Db 4.21 ATGAACTCAGTTGTTATACAAGAAATGAAATGCTATTAAATACCGATCATGAAGT 480  
 4.21 ATGAACTCAGTTGTTATACAAGAAATGAAATGCTATTAAATACCGATCATGAAGT 480

QY 481 AAAAAGTGTCAAATATGACATGAGCGTTTGTCTACCGGTATCGAGTTAGTT 540  
 481 AAAAAGTGTCAAATATGACATGAGCGTTTGTCTACCGGTATCGAGTTAGTT 540

Db 541 GGATCTCTCAAAGATTTGGCCATATTAGTTATTTGGCTTAAGCGTTTGCAA 600  
 541 GGATCTCTCAAAGATTTGGCCATATTAGTTATTTGGCTTAAGCGTTTGCAA 600

QY 601 GAGACGAGGAGAAGATGGTCAGTAACAAACAGACACTGTTAGTTGGTA 660  
 601 GAGACGAGGAGAAGATGGTCAGTAACAAACAGACACTGTTAGTTGGTA 660

Db 661 CTTGGTAGGAAGTCGATTATGGCTTAAGCGTTTGCAA 720  
 661 CTTGGTAGGAAGTCGATTATGGCTTAAGCGTTTGCAA 720

QY 721 TCGTATTAGTTGACTCTGGTAAAGTGTAGTTAACTGAGT 780  
 721 TCGTATTAGTTGACTCTGGTAAAGTGTAGTTAACTGAGT 780

Db 781 TGTGTTCATGAGGTGATGGTATTAATTGTTGACTAGGGCATTCTCACACAA 840  
 Db 781 TGTGTTCATGAGGTGATGGTATTAATTGTTGACTAGGGCATTCTCACACAA 840

QY 841 TAACAAGTTATAGATTTTTAACATTGCCCCCTGTAAGTTGGTA 900  
 Db 841 TAACAAGTTATAGATTTTTAACATTGCCCCCTGTAAGTTGGTA 900

QY 901 TTACACCGCATTTCCTGTACAAGATTCAATTGCCCCCTGTAAGTTGGTA 960  
 Db 901 TTACACCGCATTTCCTGTACAAGATTCAATTGCCCCCTGTAAGTTGGTA 960

QY 961 GACAATTATAAGTTATAACGTTTACAATTATAACCATGTGAAGATCCAAGAA 1020  
 Db 961 GACAATTATAAGTTATAACGTTTACAATTATAACCATGTGAAGATCCAAGAA 1020

QY 1021 TATGTTACTCTTCTTGTGTTAGAAAGAAACTAACTATACACTAATAATTCT 1080  
 Db 1021 TATGTTACTCTTCTTGTGTTAGAAAGAAACTAACTATACACTAATAATTCT 1080

QY 1081 AATCATATAATTGTAATATGCAATTGTTGAAATTAGTATTGAGCTAC 1140  
 Db 1081 AATCATATAATTGTAATATGCAATTGTTGAAATTAGTATTGAGCTAC 1140

QY 1141 TTATCACTTCAGCCAAATATGATTGGATTAAGTCCAAATGCAATTGTTGAGTAC 1200  
 Db 1141 TTATCACTTCAGCCAAATATGATTGGATTAAGTCCAAATGCAATTGTTGAGTAC 1200

QY 1201 CTCTTGTCGTCATAATGATTCAATTCTTAAATTCTAACACTACAGAGCTACA 1260  
 Db 1201 CTCTTGTCGTCATAATGATTCAATTCTTAAATTCTAACACTACAGAGCTACA 1260

QY 1261 TTATATTGTTCTAATGACAGGAAACTTCTCATAGAGATTAGATGAATTGTT 1320  
 Db 1261 TTATATTGTTCTAATGACAGGAAACTTCTCATAGAGATTAGATGAATTGTT 1320

QY 1321 GGGAAACATCATGAAACAGGAAACTTTGCAATCATATGATTCTACAAAGAT 1380  
 Db 1321 GGGAAACATCATGAAACAGGAAACTTTGCAATCATATGATTCTACAAAGAT 1380

QY 13.81 ACTTAGCGTAATGAAAGTCACTGTTGTAATGACTATGATTGATCAATTGTTAATT 1440  
 Db 13.81 ACTTAGCGTAATGAAAGTCACTGTTGTAATGACTATGATTGATCAATTGTTAATT 1440

QY 1441 TTGTCGATCATTTTGATTGATAAGCTTCAACTATTGATCAATTGTTCT 1500  
 Db 1441 TTGTCGATCATTTTGATTGATAAGCTTCAACTATTGATCAATTGTTCT 1500

QY 1501 TGTGATAAACAGAACTTGTAACTATTGATCAATTGTTCT 1560  
 Db 1501 TGTGATAAACAGAACTTGTAACTATTGATCAATTGTTCT 1560

QY 1561 TCCTTGTTTATGTGATTAGTTGATGCTTAAGCTTAACTTTGATGCAAGGTTCT 1620  
 Db 1561 TCCTTGTTTATGTGATTAGTTGATGCTTAAGCTTAACTTTGATGCAAGGTTCT 1620

QY 1621 AATAAACATGTCAGTAACTACGTATCACTGTTTGCCTACCGGTATCGAGTTAGTT 1680  
 Db 1621 AATAAACATGTCAGTAACTACGTATCACTGTTTGCCTACCGGTATCGAGTTAGTT 1680

QY 1681 TACTCATGATAGTTTTTGTGAAATGTCAATTAAATGCTTTTCCAAATAATTAA 1740  
 Db 1681 TACTCATGATAGTTTTTGTGAAATGTCAATTAAATGCTTTTCCAAATAATTAA 1740

QY 1741 TTAAATTAAATAAGAAATATTATGCAAAACATCATCAACACATATCCAACT 1800  
 Db 1741 TTAAATTAAATAAGAAATATTATGCAAAACATCATCAACACATATCCAACT 1800

QY 1801 TCGAAATCTCTATAGTACACAAGTAGAGAAATTTACTAGATCAACTCTCA 1860  
 Db 1801 TCGAAATCTCTATAGTACACAAGTAGAGAAATTTACTAGATCAACTCTCA 1860

QY 1861 ATCATCAATTAAATGTTACAAACTAATTAAACCCACCAAAATTAACTAAAT 1920  
 QY

Db	1861	ATCATCAATTAAATGTTACAAACTAATTAAACCCACCACTAAATAAAT	1920	Db	2941	GCGAATAAGTTCTTAAGATTGAACTCCTGTGCCGGCTTGCGATGATTATAAT	3000
QY	1921	CCGAGCAAAGTGACTGAAACAGACTGATTTCAGGTGATGAGCTAAATGGCTACG	1980	QY	3001	TCTGTGGAATTAGCTAACGTAATATTACATGTAATGCGTATTATGA	3050
Db	1921	CCGAGCAAAGTGACTGAAACAGACTGATTTCAGGTGATGAGCTAAATGGCTACG	1980	Db	3001	TCTGTGGAATTAGCTAACGTAATATTACATGTAATGCGTATTATGA	3060
QY	1981	TATCAACATCACGATCATTAGTTATGTAATGAAATGTTAGCTACTTGTAAC	2040	QY	3061	GATGGGTTTATGATTAGTAGTCCCGCAATTATACTTAAATACGGATAGAAACAAA	3120
Db	1981	TATCAACATCACGATCATTAGTTATGTAATGAAATGTTAGCTACTTGTAAC	2040	Db	3061	GATGGGTTTATGATTAGTAGTCCCGCAATTATACTTAAATACGGATAGAAACAAA	3120
QY	2041	AAAAATGCTTGATTGGATACTCACTTCATGTAACATTACATCAACCTTA	2100	QY	3121	TATGGCGCGCAAACCTGGATAATTATCGCGCGGGTGTCACTATGTTACTAGATCGAA	3180
Db	2041	AAAAATGCTTGATTGGATACTCACTTCATGTAACATTACATCAACCTTA	2100	Db	3121	TATGGCGCGCAAACCTGGATAATTATCGCGCGGGTGTCACTATGTTACTAGATCGAA	3180
QY	2101	TTTCACTATAAACCCATCTCACTGACCTCTGAAGTAATCAATTAGAGCAAAGT	2160	QY	3181	TTC 3183	
Db	2101	TTTCACTATAAACCCATCTCACTGACCTCTGAAGTAATCAATTAGAGCAAAGT	2160	Db	3181	TTC 3183	
QY	2161	CATTTAACTTCTCTAAACCATGGACCCCTGCATCTAATTTCGGTCAAACCTGACAGGA	2220	RESULT 2			
Db	2161	CATTTAACTTCTCTAAACCATGGACCCCTGCATCTAATTTCGGTCAAACCTGACAGGA	2220	ID	AAD33601		
QY	2221	AAGACGACGACGGCGATAGCTCTGCCAGCAGAGGGCTCCAGTCCCTTGCTGT	2280	ID	AAD33601; standard; DNA; 3183 bp.		
Db	2221	AAGACGACGACGGCGATAGCTCTGCCAGCAGAGGGCTCCAGTCCCTTGCTGT	2280	XX			
QY	2281	CGGGTCCAATCGTGTCTCAACTATCAACCGGAAGCGGGACGACGGCTCCAGTCCCTTGCTGT	2340	AC			
Db	2281	CGGGTCCAATCGTGTCTCAACTATCAACCGGAAGCGGGACGACGGCTCCAGTCCCTTGCTGT	2340	XX			
QY	2341	AAAGGAACGACGGCTCTACCTTGATGATCGGCTCTGGT3GAGGTATCATCGCAGCC	2400	DE	01-JUL-2002 (first entry)		
Db	2341	AAAGGAACGACGGCTCTACCTTGATGATCGGCTCTGGT3GAGGTATCATCGCAGCC	2400	XX	A. thaliana SAG12 promoter/IPT/NOS-ter construct.		
QY	2401	AAGCAAGCTCATAGGCTGATCGAGGGGTATAATCATGAGGCCAACGGGGCTT	2460	KW	Senescence associated gene; SAG-12; transgenic plant; transgenic; senescence-specific promoter; senescence characteristic; chimeric; IPT; isopentenyl transferase; NOS-ter; ds.		
Db	2401	AAGCAAGCTCATAGGCTGATCGAGGGGTATAATCATGAGGCCAACGGGGCTT	2460	KW	Arabidopsis thaliana.		
QY	2461	ATTCTGTAGGGAGATCCACCTCGTGTGATCGAGGGAGGTATAATCATGAGGCCAACGGGGCTT	2520	OS	Unidentified.		
Db	2461	ATTCTGTAGGGAGATCCACCTCGTGTGATCGAGGGAGGTATAATCATGAGGCCAACGGGGCTT	2520	OS	Chimeric.		
QY	2521	GCAGATTTCGTCATATTGCCACAAGTACCCGACCAAGAGACCTTCATGAAA	2580	XX			
Db	2521	GCAGATTTCGTCATATTGCCACAAGTACCCGACCAAGAGACCTTCATGAAA	2580	FH			
QY	2581	GCGGCCAACGGCCAGGTAAAGCATGGCTGACCCCGCTGCAACGGCATTCATTCAA	2640	Key			
Db	2581	GCGGCCAACGGCCAGGTAAAGCATGGCTGACCCCGCTGCAACGGCATTCATTCAA	2640	FT			
QY	2641	GAGTTGGTTATCTTGGATGAACTCGGCTGAGGCCATCTGAAAGAGATCGAGA	2700	FT	promoter	Location/Qualifiers	
Db	2641	GAGTTGGTTATCTTGGATGAACTCGGCTGAGGCCATCTGAAAGAGATCGAGA	2700	FT	1..2074		
QY	2701	TATGGATATGCCATGTTGCTAGCCAGAACAGATCACGGAGATGCTATGGAG	2760	FT	/*tag= a		
Db	2701	TATGGATATGCCATGTTGCTAGCCAGAACAGATCACGGAGATGCTATGGAG	2760	FT	/note= "SAG12 promoter"		
QY	2761	CTTGACGCAAATATGGAAGGTAAGTGATTAATGGATCGCTCAGGAGATTCCAT	2820	FT	2075		
Db	2761	CTTGACGCAAATATGGAAGGTAAGTGATTAATGGATCGCTCAGGAGATTCCAT	2820	FT	/*tag= b		
QY	2821	GCGGCCAACAGGAACAGAAATTCCCCAAGTTACGCAGCCGCTTCCACGGATTGAA	2880	FT	/note= "Transcription start site"		
Db	2821	GCGGCCAACAGGAACAGAAATTCCCCAAGTTACGCAGCCGCTTCCACGGATTGAA	2880	FT	2076..2179		
QY	2881	GGTOATCCGTCGGAATGTTAGGTACGCCAGCCTGAGCTCGTCACCAATT	2940	FT	/*tag= c		
Db	2881	GGTCATCCGTCGGAATGTTAGGTACGCCAGCCTGAGCTCGTCACCAATT	2940	FT	2180..2919		
QY	2941	GGCAATAAGTTCTTAAGATTCTGTGCGGCTTGCGATGATTATATAAT	3000	FT	/*tag= d		
				FT	/note= "NcoI-IPT sequence"		
				FT	2920..3183		
				FT	/*tag= e		
				FT	/note= "SstI-NOS ter sequence"		
				XX	US6359197-B1.		
				XX	19-MAR-2002.		
				XX	17-NOV-1997;	97US-00971395.	
				XX	29-MAR-1995;	95US-00413135.	
				XX	(WISC ) WISCONSIN ALUMNI RES FOUND.		
				XX	Amasino RM, Gan S, Noh Y;		
				XX	WPI; 2002-291012/33.		
				XX			
				PT	Novel senescence associated promoter sequence connected to a protein-		
				PT	coding DNA sequence useful for the creation of transgenic plants with		
				PT	altered senescence characteristics.		
				PS	Claim 1; Fig 3; 21pp; English.		
				XX			

CC	The invention relates to a genetic construct comprising senescence specific promoter, preferably senescence associated gene (SAG)-12 promoter operably connected to a protein-coding DNA sequence not natively connected to the promoter. The senescence associated promoters are useful for the creation of transgenic plants with altered senescence characteristics. Genetic constructs can be inserted into plants which become effective only upon plant cells entering senescence. For example, a gene encoding a biosynthetic enzyme under the control of a senescence-specific promoter can be inserted into a plant, without having the tissues of the plant exposed to the excess of cytokinin during pre-senescence growth. Then at the onset of senescence, the senescence-specific promoter activates cytokinin production to alter the progression of senescence in the plant. The present sequence is a chimeric construct comprising Arabidopsis thaliana SAG12 promoter, isopentenyl transferase (IPT) gene and NOS-ter sequence. Note: This sequence is stated to be same as that shown as SEQ ID NO:1 (AAD33336) in Column 15-20 of the specification. However the sequences differ at several positions	Db	721 TCGTTATTAGTRTGACTGGTACCTGGTTAAGAAAAGTGTATAGTTAACAGT	780
CC	Sequence 3183 BP; 1042 A; 528 C; 559 G; 1054 T; 0 U; 0 Other;	QY	781 TGTGTCATGAGGTGATGTGATTAATTGTTGACTAGGGCATTCCACATCAA	840
CC	Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 3180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Db	781 TGTGTCATGAGGTGATGTGATTAATTGTTGACTAGGGCATTCCACATCAA	840
QY	1 GATATCTCTTTATATTCAAACAAATAAGTGAGATATGTTGAGAAGAGGACAATT	QY	841 TAACAAAGTTAGATTTTATACATTGCACTTGCACCGTTCGTAAGTTGGA	900
Db	1 GATATCTCTTTATATTCAAACAAATAAGTGAGATATGTTGAGAAGAGGACAATT	QY	841 TAACAAAGTTAGATTTTATACATTGCACTTGCACCGTTCGTAAGTTGGA	900
QY	61 CTCGTGGAGCACCGAGCTGTTTATATTAGAAACCCGATGTTATTAGTACTGAGAC	Db	901 TTACACCGATTTCCTGACAAGATTACATTATTATTATACCTCCAGT	960
Db	61 CTCGTGGAGCACCGAGCTGTTTATATTAGAAACCCGATGTTATTAGTACTGAGAC	QY	901 TTACACCGATTTCCTGACAAGATTACATTATTATTATACCTCCAGT	960
QY	121 AAAAAGTAATCGTGATGTTAAATTAAATTAGTTCATCACGTTCGATAAA	Db	961 GACAATTATAAGTTTACAAATTATTAAATACCATGTAAGATCCAAAGAA	1020
Db	121 AAAAAGTAATCGTGATGTTAAATTAAATTAGTTCATCACGTTCGATAAA	QY	961 GACAATTATAAGTTTACAAATTATTAAATACCATGTAAGATCCAAAGAA	1020
QY	181 AATGATTAGTTATCATAGCTAATAATAGCATGTTCAATTGTTGACACCTT	Db	1021 TATGTCCTACTCTCTTGTGTAAGAAAACTAACATATCACAATAATAATTCT	1080
QY	181 AATGATTAGTTATCATAGCTAATAATAGCATGTTCAATTGTTGACACCTT	Db	1021 TATGTCCTACTCTCTTGTGTAAGAAAACTAACATATCACAATAATAATTCT	1080
Db	181 AATGATTAGTTATCATAGCTAATAATAGCATGTTCAATTGTTGACACCTT	QY	1081 AATCATTATATTGTAATAATGCAATTGTCATTGAAATTAGTATTGTCATTGACGG	1140
QY	241 TTTCTCTCTTGGTTCTAACATTAGAGAACCCATAACAATGTCAAATT	Db	1081 AATCATTATATTGTAATAATGCAATTGTCATTGAAATTAGTATTGTCATTGACGG	1140
Db	241 TTTCTCTCTTGGTTCTAACATTAGAGAACCCATAACAATGTCAAATT	QY	1141 TTATCACTCAGCCAATATGATTGGTTAACCTTCAACTACAGAGCTACA	1200
QY	301 AATTAAACAAATATTCCAAGTTTATATGAAACAGTT 360	Db	1141 TTATCACTCAGCCAATATGATTGGTTAACCTTCAACTACAGAGCTACA	1200
Db	301 AATTAAACAAATATTCCAAGTTTATATGAAACAGTT 360	QY	1201 CTCTGTGCTATGATTTCATAGTAAATTCTTATATTACCTTAACTACAGAGCTACA	1260
QY	361 GAATAGTTGATTATGAAATTAGTCAATCTCAATTGATGTTATAT	Db	1201 CTCTGTGCTATGATTTCATAGTAAATTCTTATATTACCTTAACTACAGAGCTACA	1260
Db	361 GAATAGTTGATTATGAAATTAGTCAATCTCAATTGATGTTATAT	QY	1261 TTATATTGTTCTAACATTGATTTCATAGGAAACTTTCAATTGTTGTT	1320
QY	421 ATGAACTCAGTTGTTATACAAGAAATGAAATGCTATTAAATACCGATCATGAGTT	Db	1261 TTATATTGTTCTAACATTGATTTCATAGGAAACTTTCAATTGTTGTT	1320
Db	421 ATGAACTCAGTTGTTATACAAGAAATGAAATGCTATTAAATACCGATCATGAGTT	QY	1321 GGGAAACATCATGAACTAGGAAACTTTAGCAATCATATCGATTATCACAAGAA	1380
QY	481 AAAAGTGTCAAGATATGACATGAAGCGTTGCTTACCGGGATCGAGTTAGGTT	Db	1321 GGGAAACATCATGAACTAGGAAACTTTAGCAATCATATCGATTATCACAAGAA	1380
Db	481 AAAAGTGTCAAGATATGACATGAAGCGTTGCTTACCGGGATCGAGTTAGGTT	QY	1381 ACTTAGCGTAATGAACTTCAGGAAACTTTAGCAATCATATCGATTATCACAAGAA	1380
QY	541 GGATCTCAAGAATATTGGGCCATTAGTTATTTGGCTTAAGGACACTCGTATTG	Db	1381 ACTTAGCGTAATGAACTTCAGGAAACTTTAGCAATCATATCGATTATCACAAGAA	1380
Db	541 GGATCTCAAGAATATTGGGCCATTAGTTATTTGGCTTAAGGACACTCGTATTG	QY	1441 TTGTCGAATCATTTCTTGTGATTGAACTTCAACTATGATTGTCATTGAAATTGTTA	1440
QY	601 GAGACGAGAAGATGGTCAAGTTAACAAACAGAGACACTCGTATTG	Db	1441 TTGTCGAATCATTTCTTGTGATTGAACTTCAACTATGATTGTCATTGAAATTGTTA	1440
Db	601 GAGACGAGAAGATGGTCAAGTTAACAAACAGAGACACTCGTATTG	QY	1501 TGTGATAAACAGAAATCTTGTGATTGAACTTCAACTATGATTGTCATTGAAATTGTTA	1500
QY	661 CTTTGGTAGCAAGTCGATTATTGCGAGTAAACTGGTACACAACCGTA	Db	1501 TGTGATAAACAGAAATCTTGTGATTGAACTTCAACTATGATTGTCATTGAAATTGTTA	1500
Db	661 CTTTGGTAGCAAGTCGATTATTGCGAGTAAACTGGTACACAACCGTA	QY	1561 TCCTGTTTTATGTGATTGTTGAACTTCAACTATGATTGTCATTGAAATTGTTA	1620
QY	721 TCGTTATTAGTTGACTGGTACCTTTGGTTAAGAAAAGTGTATAGTTAAC	Db	1561 TCCTGTTTTATGTGATTGTTGAACTTCAACTATGATTGTCATTGAAATTGTTA	1620
QY	721 TCGTTATTAGTTGACTGGTACCTTTGGTTAAGAAAAGTGTATAGTTAAC	QY	1621 AAATAACATGTCAGTAACTACGTTACCATGTTAAAGTATTTCACAAATTAA	1680
Db	721 TCGTTATTAGTTGACTGGTACCTTTGGTTAAGAAAAGTGTATAGTTAAC	QY	1621 AAATAACATGTCAGTAACTACGTTACCATGTTAAAGTATTTCACAAATTAA	1680
QY	1681 TACTCATGATAGTTTTTGTAAATGCAATTAAATGCTTCTTAATTAA	Db	1681 TACTCATGATAGTTTTTGTAAATGCAATTAAATGCTTCTTAATTAA	1740
Db	1681 TACTCATGATAGTTTTTGTAAATGCAATTAAATGCTTCTTAATTAA	QY	1741 TTTATAATAAGGAAATTATGCAACACATCAACACATCCACT	1800
QY	1741 TTTATAATAAGGAAATTATGCAACACATCAACACATCCACT	Db	1741 TTTATAATAAGGAAATTATGCAACACATCAACACATCCACT	1800
Db	1741 TTTATAATAAGGAAATTATGCAACACATCAACACATCCACT	QY	1801 TCGAAAATCTCTAGTACCAAGTAGAGAAATTAACTAGATACAAACTTCCTA	1860

Db	1801	TCGAAATCTCTAGTACACAAGTAGAGAAATAATTACTAGATACAACTTCCA	1850	QY	2941	GGCAATAAGTTCTTAAGATTGAATCCTGTGCCGGCTTGCGATGATATCATATAAT	3000
QY	1861	ATCATCAATTAAATGTTACAACATAATTAAACCCACCAATTAACTAAAT	1920	Db	2941	GGCAATAAGTTCTTAAGATTGAATCCTGTGCCGGCTTGCGATGATATCATATAAT	3000
Db	1861	ATCATCAATTAAATGTTACAACATAATTAAACCCACCAATTAACTAAAT	1920	QY	3001	TTCTGTGAATTACGTTAAGCATGTAATAATTAACTGTAATGCGATGACTTATGAA	3060
QY	1921	CCGAGCAAAGTGAACAGACTGATTGAGTTAGCTAGGTTAGACTAAATGGCTAC	1980	Db	3001	TTCTGTGAATTACGTTAAGCATGTAATAATTAACTGTAATGCGATGACTTATGAA	3060
Db	1921	CCGAGCAAAGTGAACAGACTGATTGAGTTAGCTAGGTTAGACTAAATGGCTAC	1980	QY	3061	GATGGTTTATGATAGAGTCCCACATTACATTAACGCGATAGAACAAA	3120
QY	1981	TATCAACATCAACGATCATTAGTTATGAAATGATGTAGCTACTTGTAAAC	2040	Db	3061	GATGGTTTATGATAGAGTCCCACATTACATTAACGCGATAGAACAAA	3120
Db	1981	TATCAACATCAACGATCATTAGTTATGAAATGATGTAGCTACTTGTAAAC	2040	QY	3121	TATGGGCCAACTGGATAATTATCGGGGGTGCATCTATGTTACTAGATCGAA	3180
QY	2041	AAAAATGCTTGGATCACTCAGTACCCCTCTGAAGTAATCAACCTTA	2100	Db	3121	TATGGGCCAACTGGATAATTATCGGGGGTGCATCTATGTTACTAGATCGAA	3180
Db	2041	AAAATGCTTGGATCACTCAGTACCCCTCTGAAGTAATCAACCTTA	2100	QY	3181	TTC 3183	3180
QY	2101	TTTCACTATAAACCCATCTCAGTACCCCTCTGAAGTAATCAACCTTA	2160	Db	3181	TTC 3183	3180
QY	2161	CATTTAECTTCTAAACCATGGACCTGCATCTAATTTCGGCCAATTGCAACAGGA	2220	RESULT 3			
Db	2161	CATTTAECTTCTAAACCATGGACCTGCATCTAATTTCGGCCAATTGCAACAGGA	2220	AAD33336			
QY	2221	AAGACGACGACCGCGATAGCTCTACCTGATGACGGCTCCAGTCCAGT	2280	ID	AAD33336		
Db	2221	AAGACGACGACCGCGATAGCTCTACCTGATGACGGCTCCAGTCCAGT	2280	XX			
QY	2281	CGGCTCAAATGTCCTCAACTATCAACCGGAAGCGGACGACCAACAGTGAAGAAGCTG	2340	AC	AAD33336;		
Db	2281	CGGCTCAAATGTCCTCAACTATCAACCGGAAGCGGACGACCAACAGTGAAGAAGCTG	2340	XX			
QY	2341	AAAGGAACGACCGCTCTACCTGATGACGGCTCTGGAGGGTATCATCGCAGCC	2400	DE	A. thaliana SAG12 promoter/IPT/NOS-ter construct (alternative version)		
Db	2341	AAAGGAACGACCGCTCTACCTGATGACGGCTCTGGAGGGTATCATCGCAGCC	2400	XX			
QY	2401	AAGCAAGCTCATAGGCTGATCCAGGAGGTATAATCATGAGGCCAACGGGGCT	2460	KW	Senescence associated gene; SAG-12; transgenic plant; transgenic; IPT; senescence-specific promoter; senescence characteristic; chimeric; IPT; isopentenyl transferase; NOS-ter; ds.		
Db	2401	AAGCAAGCTCATAGGCTGATCCAGGAGGTATAATCATGAGGCCAACGGGGCT	2460	KW			
QY	2461	ATTCTTGAGGGAGATCCACCTCGTTGCTCACTGCATGGGCCAACGGGGCT	2520	OS	Arabidopsis thaliana.		
Db	2461	ATTCTTGAGGGAGATCCACCTCGTTGCTCACTGCATGGGCCAACGGGGCT	2520	OS	Unidentified.		
QY	2521	GCAGATTTCGTTGGCATATTTCGCCACAGTTACCCGACCAAGACCTTCATGAA	2580	OS	Chimeric.		
Db	2521	GCAGATTTCGTTGGCATATTTCGCCACAGTTACCCGACCAAGACCTTCATGAA	2580	XX			
QY	2581	GCGGCCAAGGCCAGAGTTAACCTCGGTGACCCGCTGCAAGGCCATTCTGAAGAAGATCGATGAA	2640	PD	US6359197-B1.		
Db	2581	GCGGCCAAGGCCAGAGTTAACCTCGGTGACCCGCTGCAAGGCCATTCTGAAGAAGATCGATGAA	2640	XX			
QY	2641	GAGTTGGTTATCTTGAAGCAGGTTAACCTCGGTGACCCGCTGCAAGGCCATTCTGAAGAAGATCGATGAA	2700	PR	19-MAR-2002.		
Db	2641	GAGTTGGTTATCTTGAAGCAGGTTAACCTCGGTGACCCGCTGCAAGGCCATTCTGAAGAAGATCGATGAA	2700	XX			
QY	2701	TATCGATATGCCATGTTGCTAGCCAGAACGATCACGGCAGATATGCTATGCA	2760	PT	17-NOV-1997; 97US-00971395.		
Db	2701	TATCGATATGCCATGTTGCTAGCCAGAACGATCACGGCAGATATGCTATGCA	2760	PT	(WISC ) WISCONSIN ALUMNI RES FOUND.		
QY	2761	CTTGACGCAAATATGGAAGGTAAATGGGATCGCTAGGAGTATTCATCAT	2820	PT	Amasino RM, Gan S, Noh Y;		
Db	2761	CTTGACGCAAATATGGAAGGTAAATGGGATCGCTAGGAGTATTCATCAT	2820	PT	WPI; 2002-291012/33.		
QY	2821	GCGGCCAACAGAACAGAACCTCCAAAGTTAACCGAGCCGCTTGAGGATTCGAA	2880	PT	Novel senescence associated promoter sequence connected to a protein-coding DNA sequence useful for the creation of transgenic plants with altered senescence characteristics.		
Db	2821	GCGGCCAACAGAACAGAACCTCCAAAGTTAACCGAGCCGCTTGAGGATTCGAA	2880	PT	Claim 1; Col 15-20; 21pp; English.		
QY	2881	GGTCATCCGTTCGGAATTAGGTTACGCCAGCCCTGAGCTCGTCACACATT	2940	PS	The invention relates to a genetic construct comprising senescence specific promoter, preferably senescence associated gene (SAG)-12 promoter operably connected to a protein-coding DNA sequence not natively connected to the promoter. The senescence associated promoters are useful for the creation of transgenic plants with altered senescence characteristics. Genetic constructs can be inserted into plants which become effective only upon plant cells entering senescence. For example, a gene encoding a biosynthetic enzyme under the control of a senescence-specific promoter can be inserted into a plant, without having the tissues of the plant exposed to the excess of cytokinin during pre-senescence growth. Then at the onset of senescence, the senescence-specific promoter activates cytokinin production to alter the progression of senescence in the plant. The present sequence is an alternative		
Db	2881	GGTCATCCGTTCGGAATTAGGTTACGCCAGCCCTGAGCTCGTCACACATT	2940	XX			



Db	1981 TATCAAACATCAACGATCATTTAGTTATGATGATGTCATTACTGTAAAC 2040	QY	3121 TATGGCGCCAACTGGATAATTATCGGCCGCGTCACTATGTTACTAGATCGAA 3180
QY	2041 AAAATGCTTGGATCAATCACTCTGAACTTACATCACACCTTA 2100	Db	3120 TATGGCGCCAACTGGATAATTATCGGCCGCGTCACTATGTTACTAGATCGAA 3179
Db	2041 AAAATGCTTGGATCAATCACTCTGAACTTACATCACACCTTA 2100	QY	3181 TTC 3183
Db	2101 TTTCACTATAACCCATCTCAGTACCCCTCTGAAGTAATCAAATTAGGCAAAGT 2160	Db	3180 TTC 3182
QY	2161 CATTTAECTTCTAAACCATGGACCCCTGCATCTAATTTCGGCCAACCTGCACAGGA 2220	RESULT 4	
Db	2161 CATTTAECTTCTAAACCATGGACCCCTGCATCTAATTTCGGCCAACCTGCACAGGA 2219	AAV69757	
QY	2221 AAGACGACGACCCTGCTAAACCATGGA-CCTGCATCTTCGGCCAACCTGCACAGGA 2280	ID	AAV69757 standard; DNA; 745 BP.
Db	2220 AAGACGACGACCCTGCTAAACCATGGA-CCTGCATCTTCGGCCAACCTGCACAGGA 2279	XX	
QY	2281 CGGGTCCAATCGTGCTCTAACATCAACCGGAAGGGACAGGGCTCCAGTCGCTTGAT 2280	AC	AAV69757;
Db	2280 CGGGTCCAATCGTGCTCTAACATCAACCGGAAGGGCTCCAGTCGCTTGAT 2279	XX	
QY	2291 AAGACGACGACCCTGCTAAACCATGGACAGGGCTCCAGTCGCTTGAT 2339	XX	01-MAR-1999 (first entry)
Db	2291 AAGACGACGACCCTGCTAAACCATGGACAGGGCTCCAGTCGCTTGAT 2339	DE	Isopentenyl transferase ipt gene.
QY	2341 AAAGGAACGACGCGCTCTACCTGATGATCGGGCTCTGGGGTATCATCGCAGCC 2400	XX	Isopentenyl transferase; ipt gene; cytokinin; transgenic plant;
Db	2340 AAAGGAACGACGCGCTCTACCTGATGATCGGGCTCTGGGGTATCATCGCAGCC 2399	OS	seedless fruit; tomato; watermelon; cucumber; ds.
QY	2401 AAGCAAGCTCATCATAGGCTGATCGAGGAGGTATAATCATGAGGCCAACGGGGCT 2460	KW	Agrobacterium tumefaciens.
Db	2400 AAGCAAGCTCATCATAGGCTGATCGAGGAGGTATAATCATGAGGCCAACGGGGCT 2459	XX	
QY	2461 ATTCTTGAGGAGGATCCACCTCGTTGCTCACTGCATGGGCCAACAGCTATTGGAGT 2520	FH	
Db	2460 ATTCTTGAGGAGGATCCACCTCGTTGCTCACTGCATGGGCCAACAGCTATTGGAGT 2519	FT	
QY	2521 GCAGATTTCGTTGCATATTTCGCCACAAGTTACCGACAGAGACCTCATGAA 2580	PR	
Db	2520 GCAGATTTCGTTGCATATTTCGCCACAAGTTACCGACAGAGACCTCATGAA 2579	XX	
QY	2581 GCGGCCAAGGCCAGAGTTAACCGAGATGTCACCCGGCTGCAGGCCATTCTCAA 2640	PA	(UNIV ) UNIV KANSAS STATE RES FOUND.
Db	2580 GCGGCCAAGGCCAGAGTTAACCGAGATGTCACCCGGCTGCAGGCCATTCTCAA 2639	XX	
QY	2641 GAGTTGGTTATCTTGGATGAACTCGGCTGAGGCCATTCTGAAGAGATCGATGGA 2700	PI	
Db	2640 GAGTTGGTTATCTTGGATGAACTCGGCTGAGGCCATTCTGAAGAGATCGATGGA 2699	XX	
QY	2701 TATCGATATGCCATGTTGCTAGCCAGAACCGATCACGGAGATATGCTATGCAG 2760	DR	WPI; 1999-034673/03.
Db	2700 TATCGATATGCCATGTTGCTAGCCAGAACCGATCACGGAGATATGCTATGCAG 2759	XX	P-PSDB; AAW81575.
QY	2761 CTTGACGCAATATGGAAAGGTAAAGGTATGGATCGCTCAGGAGTATTCCAT 2820	PT	A new construct to express phytohormones in developing fruit - useful
Db	2760 CTTGACGCAATATGGAAAGGTAAAGGTATGGATCGCTCAGGAGTATTCCAT 2819	PT	for, e.g. producing substantially seedless fruit from transgenic plants.
QY	2821 GCGGCCAACAGGAACAGAAATCCCCAACGTTACCGACGCCCTTCGACGGATTCCAA 2880	PS	Example 1; Page 31-33; 49pp; English.
Db	2820 GCGGCCAACAGGAACAGAAATCCCCAACGTTACCGACGCCCTTCGACGGATTCCAA 2879	XX	This is the nucleotide sequence of the Agrobacterium tumefaciens ipt gene that codes for isopentenyl transferase (see AAW81575), an enzyme of the cytokinin biosynthetic pathway. A claimed DNA construct comprises either an isopentenyl transferase or a tryptophan oxygenase (see AAW81574) encoding sequence, operably linked to an ovary or developing fruit-specific plant-expressible promoter (see AAV69755 and AAV69759). The construct is used to stably integrate enzymes involved in cytokinin or auxin biosynthesis into the plant genome to achieve a transgenic plant (preferably tomato, cucumber or watermelon) producing seedless fruit in the absence of pollination.
QY	2881 GGTCTATCCGTTCGGAATGTTAGGTACGCCAGCCCTGAGCTCGATCGTCAACATT 2940	CC	Sequence 745 BP; 193 A; 185 C; 192 G; 175 T; 0 U; 0 other;
Db	2880 GGTCTATCCGTTCGGAATGTTAGGTACGCCAGCCCTGAGCTCGATCGTCAACATT 2939	CC	
QY	2941 GGCATAAAGTTCTAAGATGATCTGTCGGGCTTGGATGATTCATAAT 3000	CC	Query Match 23.1%; Score 734.8; DB 2; Length 745;
Db	2940 GGCATAAAGTTCTAAGATGATCTGTCGGGCTTGGATGATTCATAAT 2999	CC	Best Local Similarity 99.7%; Pred. No. 2.4e-114; Matches 736; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	3001 TTCTGTTGAATTACGTTAAGCATGTAATAACATGTAATGCACTTC 3060	QY	2187 CCTGCATCTAATTTCGGTCAACTTGACAGGAAGACGACCGCGATAGCTCTGC
Db	3000 TTCTGTTGAATTACGTTAAGCATGTAATAACATGTAATGCACTTC 3059	Db	2247 CCAGCAGACAGGCTCCAGTCCCTTCGCTGATCGGCTCAACTTGACAGGTCTGC
QY	3061 GATGGTTTATGATAGTCCCGCAATTACATTAATACGGATAGAAAACAAA 3120	QY	68 CCTGCATCTAATTTCGGTCAACTTGACAGGAAGACGACCGCGATAGCTCTGC
Db	3060 GATGGTTTATGATAGTCCCGCAATTACATTAATACGGATAGAAAACAAA 3119	Db	67 CCAGCAGACAGGCTCCAGTCCCTTCGCTGATCGGCTCAACTTGACAGGTCTGC

QY	2307	AACCGGAAGCGGACCAACAGTGGAAAGAACTGAAAGGAACCGGCGTCCTACCTTGA	2366	XX	Spangenber G, Lin YH, Parish RW, Li SF, Heazlewood J;
Db	128	AACCGGAAGCGGACCAACAGTGGAAAGAACTGAAAGGAACCGGCGTCCTACCTTGA	187	PI	Pallaghy CK;
DR				XX	WPI; 2002-304382/34.
XX				PT	Manipulating plant senescence, useful e.g. for increasing shelf life of fruit, comprises expressing gene involved in cytokine synthesis under control of myb gene promoter.
PS				PT	Claim 7; Fig 2; 27pp; English.
XX				CC	The invention describes a method of manipulating senescence in a plant comprising introducing a genetic construct that includes a myb gene promoter linked to a gene encoding an enzyme involved in biosynthesis of a cytokinin, where both the promoter and the gene may be used as functionally active fragments or variants. Manipulation (specifically delay) of senescence is used to increase shelf life of fruits, flowers, leaves and tubers in horticultural produce and cut flowers, reduce perishability of horticultural crops, improve carbon fixation (and thus yield, including biomass in forage crops) and increase seed production.
CC				CC	Use of the myb gene promoter (unlike other promoters used for overexpression of the cytokinin biosynthesis gene) does not cause retarded root and shoot growth, failure of root formation, reduced apical dominance and reduced leaf area. This sequence represents the Agrobacterium tumefaciens isopentenyl transferase (ipt) gene, the product of which is involved in cytokinin biosynthesis
CC				CC	
CC				CC	
CC				CC	
CC				CC	
CC				CC	
CC				CC	
CC				CC	
XX		Sequence 1988 BP; 593 A; 386 C; 406 G; 603 T; 0 U; 0 Other;		SQ	
Query	Match	23.0%; Score 733.4; DB 6; Length 1988;		Query	
Db	ID	Best Local Similarity 96.0%; Pred. No. 4.3e-114; Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;		Db	
QY	ABK12492	ABK12492 standard; DNA; 1988 BP.		QY	2139 TAATCAAATTAAAGAGCAAAGTCATTAACCTTCTAAACCATTGGAACCTGCATCTAAT
XX				Db	647 TAATATAAAATCAGTTGTATTCAATAACTGCAAAACCTTATGGACCTGCATCTAAT
AC				QY	2199 TTTCGGTCCAACTTGCACAGGAAGAGCACGCCGATAGCTCTGCCAGCAGACGG
XX				Db	707 TTTCGGTCCAACTTGCACAGGAAGAGCACGCCGATAGCTCTGCCAGCAGACGG
DT				QY	2259 GCTTCCAGTCTTCGCTGATGGGTCAAATCGTGTCCTCAACTATCAACCGGAAGCGG
XX				Db	767 GCTTCCAGTCTTCGCTGATGGGTCAAATCGTGTCCTCAACTATCAACCGGAAGCGG
DE				QY	2319 ACGACCAAACAGTGGAGAACTGAAGAACCGACGCCGCTCTACCTTGATGATCGGCC
XX				Db	827 ACGACCAAACAGTGGAGAACTGAAGAACCGACGCCGCTCTACCTTGATGATCGGCC
XX		18-JUN-2002 (first entry)		QY	2379 GGTGGAGGTATCATGCCAGCCAAGCAAGCTCATCATGGCTGATGGAGGTATAA
AC	ABK12492;			Db	887 GGTGGAGGTATCATGCCAGCCAAGCAAGCTCATGGCTGATGGAGGTATAA
XX				QY	2439 TCATGAGGCCAACGGGGCTTATTCTGAGGGATCCACCTCGTGCTCACTGCAT
XX				Db	947 TCATGAGGCCAACGGGGCTTATTCTGAGGGATCCACCTCGTGCTCACTGCAT
KW	Agrobacterium tumefaciens isopentenyl transferase (ipt) gene.			QY	2499 GGCGCGAACAGCTATTGGAGTCAGATTCTGGCATATTGCCACAGTTAC
KW	Isopentenyl transferase; ipt; myb32; promoter; transgenic; plant; senescence; cytokinin biosynthesis; shelf life; fruit; flower; leaf; tuber; horticulture; carbon fixation; biomass; forage crop; seed production; root growth; shoot growth; root formation; apical dominance; gene; ds.			Db	1007 GGCGCGAACAGCTATTGGAGTCAGATTCTGGCATATTGCCACAGTTAC
KW				QY	2559 CGACCAAGAGACCTCATGAAAGCGGCCAGGTTAACAGATGTTGGATGAA
XX	Arabidopsis thaliana.			Db	1067 CGACCAAGAGACCTCATGAAAGCGGCCAGGTTAACAGATGTTGGATGAA
XX				QY	2619 TGCAGGCCATTCTATTCAAGAGTTGGTTATCTTGGATGAACTCGGCTGAGGCC
PD	14-MAR-2002.			Db	1127 TGCAGGCCATTCTATTCAAGAGTTGGTTATCTTGGATGAACTCGGCTGAGGCC
XX				PR	06-SEP-2000; 2000AU-0000946.
XX				PA	(AGRIT-) AGRIC VICTORIA SERVICES PTY LTD.

Db	1187 CATTCTGAAGAGATCGATGGATATGCCATGTTGCTAGCCAGAACAGAT	1246	QY	2139 TAATCAATAAGGCAGAAAGTCATTAACTTCTAAACCATGGACCCCTGCATCTAAT	2198
QY	2739 CACGGCAGATATGCTATTGCAAGGCAAATATGGAAGGTAAATTGGGAT	2798	Db	8728 TAATATAAAATCAGTTTGTATTCAATATACTGCAGAAAACATTATGGACCTGCATCTAAT	8787
Db	1247 CACGGCAGATATGCTATTGCAAGGCAAATATGGAAGGTAAATTGGGAT	1306	QY	2199 TTTGGTCCAACCTTGCACAGGAAGACGAGCACGGCGATAGCTCTGCCAGCAGAGG	2258
QY	2799 CGCTCAGGAGTATTTCATCCATGCCAACAGGAACAGAAATTCCCCAAGTTAACGC	2858	Db	8788 TTTCGGTCCAACCTTGCACAGGAAGACGAGCACGGCGATAGCTCTGCCAGCAGAGG	8847
Db	1307 CGCTCAGGAGTATTTCATCCATGCCAACAGGAACAGAAATTCCCCAAGTTAACGC	1366	QY	2259 GCTTCAGTCTTCGCTTGATCGGGTCCAACTGTGTTCTCAACTATCACCGGAAGGG	2318
QY	2859 AGCCGCTTCGACGGATTGAAAGGTATCGCTGGAAATGTTACGCCAGCCCT	2918	Db	8848 GCTTCAGTCTTCGCTTGATCGGGTCCAACTGTGTTCTCAACTATCACCGGAAGGG	8907
Db	1367 AGCCGCTTCGACGGATTGAAAGGTATCGCTGGAAATGTTACGCCAGCCCT	1426	QY	2319 ACGACCAACAGTGGAGAACTGAAAGGAACGACGGCTACCTTGATGTCGGCCT	2378
QY	2919 GAG 2921		Db	8908 ACGACCAACAGTGGAGAACTGAAAGGAACGACGGCTACCTTGATGTCGGCCT	8967
Db	1427 GCG 1429		QY	2379 GGTGGAGGTATCATGCCAGCAAGCAAGCTCATCATGGCTGATCGAGGGTGTATAA	2438
	RESULT 6		Db	8968 GGTGGAGGTATCATGCCAGCAAGCTCATCATGGCTGATCGAGGGTGTATAA	9027
ID	AAN50182 standard; DNA; 24596 BP.		QY	2439 TCATGAGGCCAACGGGGCTATTCTGAGGGATCCACCTCGTCACTGCT	2498
XX			Db	9028 TCATGAGGCCAACGGGGCTATTCTGAGGGATCCACCTCGTCACTGCT	9087
AC			QY	2499 GGGCGGAAACAGCTATTGGAGTCAGATTTCGTTGAGGATCCACCTCGTCACTGCT	2558
XX			Db	9088 GGGCGGAAACAGCTATTGGAGTCAGATTTCGTTGAGGATCCACCTCGTCACTGCT	9147
DE	Complete nucleotide sequence of the T-DNA region of the octopine Ti plasmid pti15955.		QY	2559 CGACCAAGAGACCTTCATGAAGGGCAAGGCCAGAGTAACGAGATGGCACCCGC	2618
DE			Db	9148 CGACCAAGAGACCTTCATGAAGGGCAAGGCCAGAGTAACGAGATGGCACCCGC	9207
XX			QY	2619 TGCAGGGCATTCTATTATTCAGAAAGGGCAAGGCCAGAGTAACGAGATGGCACCCGC	2678
KW	Plant vector; transformation-inducing principle (TIP) gene; octopine Ti plasmid; ss.		Db	9208 TGCAGGGCATTCTATTATTCAGAAAGGGCAAGGCCAGAGTAACGAGATGGCACCCGC	9267
XX			QY	2679 CATTCTGAAGAGATCGATGGATATGCCATGTTGTTGCTAGCCAGAACAGAT	2738
OS	Agrobacterium tumefaciens; ATCC 15955.		Db	9268 CATTCTGAAGAGATCGATGGATATGCCATGTTGTTGCTAGCCAGAACAGAT	9327
XX			QY	2739 CACGGCAGATATGCTATTGCAAGGCAAATATGGAAGGTAAATTGGGAT	2798
PD			Db	9328 CACGGCAGATATGCTATTGCAAGGCAAATATGGAAGGTAAATTGGGAT	9387
XX			QY	2799 CGCTCAGGAGTATTTCATCCATGCCAACAGGAACAGAAATTCCCCAAGTTAACGC	2858
PA	(AGRK ) AGRIGENETICS RES ASSOC LTD.		Db	9388 CGCTCAGGAGTATTTCATCCATGCCAACAGGAACAGAAATTCCCCAAGTTAACGC	9447
PA	(LUBR ) LUBRIZOL GENETICS INC.		QY	2859 AGCCGCTTCGACGGATTGAAAGGTATCGCTGGATGTTAGGTGTGCTAGCC	2918
XX			Db	9448 AGCCGCTTCGACGGATTGAAAGGTATCGCTGGATGTTAGGTGTGCTAGCC	9507
PI	Barker RF, Kemp JD;		QY	2919 GAG 2921	
XX			Db	9508 GCG 9510	
PR	18-NOV-1984; 84EP-00307969.				
XX					
PF					
XX					
PS	Claim 28; Fig 1; 87pp; English.				
XX					
CC	The inventors claim a vector contg. a transformation-inducing principle (TIP) gene from Ti plasmid pti15955. The sequence of the T-DNA of the				
CC	octopine-type Ti plasmid has fourteen open reading frames bounded by eukaryotic promoters, ribosome binding sites, and polyadenylation sites.				
CC	With the vectors, expression of structural foreign genes in plant cells is promoted. The gene esp. encodes an insecticidal toxin identical to one derived from the crystal protein of Bacillus thuringiensis. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)				
CC					
SQ	Sequence 24596 BP; 6534 A; 5510 C; 5793 G; 6759 T; 0 U; 0 Other;				
	Query Match 23.0%; Score 733.4; DB 1; length 24596;				
	Best Local Similarity 96.0%; Pred. No. 4.9e-114;				
	Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;				



Matches	716;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;	PR	05-NOV-1998;	98US-0107185P.																																																																																																																																																																																																																																																																																																																																																																																																																										
QY	2187	CCTGCATCTAATTTCGGTCCAACCTGCCACAGGAAGACGACCGCGATAAGCTCTTG	2246	PA	XX						(UYOR-) UNIV OREGON STATE.																																																																																																																																																																																																																																																																																																																																																																																																																											
QY	6	CCTGCATCTAATTTCGGTCCAACCTGCCACAGGAAGACGACCGCGATAAGCTCTTG	65	PA	XX																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	2247	CCAGCAGACAGGGCTTCAGTCCTTCGCTTGATCGGGCCAATCGTGTGTCCTCAACTTC	2306	DR	XX																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	66	CCAGCAGACAGGGCTTCAGTCCTTCGCTTGATCGGGCCAATCGTGTGTCCTCAACTTC	125	PT	XX																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	2307	AACCGGAAGCGGACGACCAACAGTGGAAAGACTGAAGAACGACGGCGCTCTACCTTG	2366	PS	XX																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	126	AACCGGAAGCGGACGACCAACAGTGGAAAGACTGAAGAACGACGGCGCTCTACCTTG	185	CC	XX																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	2367	TGATCGGCCTCTGGCGAGGTTATCATCGCAGCCAAGCGCTTATTCGAGGCTTACCTTG	2426	CC	XX																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	186	TGATCGGCCTCTGGCGAGGTTATCATCGCAGCCAAGCGCTTACCTTG	245	CC	XX																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	2427	GGAGGGTATAATCATGAGGCCAACGGGGCTTATTCGAGGATCCACCTCG	2486	CC	XX																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	2487	GCTCAACTGCATGGCGCGAACAGCTATTGGAGTCAGATTTCGAGGATTTG	2546	CC	XX																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	306	GCTCAACTGCATGGCGCGAACAGCTATTGGAGTCAGATTTCGAGGATTTG	365	CC	XX																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	2547	CCACAAAGTTACCCGACCAGAGACCTTCATGAAAGCGGCCAAGGCCAGAGTAAGCAG	2606	CC	XX																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	366	CCACAAAGTTACCCGACCAGAGACCTTCATGAAAGCGGCCAAGGCCAGAGTAAGCAG	425	CC	XX																																																																																																																																																																																																																																																																																																																																																																																																																																	
QY	2607	GTGCAACCCGCTGCAGGCCATTCTTCAAGAGTTGTTATCTTGAAATGACC	2666	SQ	Sequence 747 BP; 198 A; 178 C; 192 G; 179 T; 0 U; 0 Other;																																																																																																																																																																																																																																																																																																																																																																																																																																	
Db	426	GTGCAACCCGCTGCAGGCCATTCTTCAAGAGTTGTTATCTTGAAATGACC	485	Query Match	22.4%	Score 712.2;	DB 3;	Length 747;																																																																																																																																																																																																																																																																																																																																																																																																																														
QY	2667	TGGCTGAGGCCATTCTGAAAGAGATCGATGGATATCGATATGCCATGTTGCTAG	2726	Best Local Similarity	99.6%	Pred. No. 1.5e-110;																																																																																																																																																																																																																																																																																																																																																																																																																																
Db	485	TGGCTGAGGCCATTCTGAAAGAGATCGATGGATATCGATATGCCATGTTGCTAG	545	Matches	714;	Conservative	0;	Mismatches	3;	Indels	0;																																																																																																																																																																																																																																																																																																																																																																																																																											
QY	2727	CCAGAACGATCACGGAGATATGCTATGCGCAAATATGGAAGGTAAGT	2786	QY	2188	CTGCATCTAATTTCGGTCCAACCTGCACAGGAAGACGACGCCGATAGCTCTGCC	2247	QY	2248	CAGCAGACGGCTCCAGTCCCTCGCTTGATCGGTCAAATCGTGTCTCACTATCA	2307	QY	2308	ACCGGAAGCGGACGACCAACAGTGGAAAGACTGAAGAACGACGCCGATAGCTCTGCC	2367	QY	2368	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	2427	QY	2428	GAGGTGTATAATCATGAGGCCAACGGGGCTTCTTGAGGGAGGATCCACCTCGTG	2487	QY	2488	CTCAACTGCATGGCGGAAACAGCTATTGGAGTCAGATTCTGAGGATCCACCTCGTG	2547	QY	258	GAGGTGTATAATCATGAGGCCAACGGGGCTTCTTGAGGATCCACCTCGTG	317	QY	2548	CTCAACTGCATGGCGGAAACAGCTATTGGAGTCAGATTCTGAGGATCCACCTCGTG	377	Db	138	CAGCAGACGGCTCCAGTCCCTCGCTTGATCGGTCAAATCGTGTCTCACTATCA	137	Db	198	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	197	Db	199	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	200	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	201	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	202	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	203	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	204	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	205	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	206	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	207	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	208	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	209	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	210	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	211	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	212	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	213	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	214	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	215	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	216	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	217	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	218	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	219	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	220	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	221	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	222	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	223	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	224	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	225	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	226	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	227	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	228	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	229	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	230	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	231	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	232	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	233	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	234	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	235	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	236	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	237	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	238	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	239	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	240	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	241	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	242	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	243	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	244	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	245	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	246	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	247	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	248	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	249	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	250	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	251	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	252	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	253	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	254	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	255	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	256	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	257	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	258	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	259	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	260	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	261	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	262	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	263	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	264	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	265	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	266	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	267	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	268	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	269	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	270	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	271	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	272	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	273	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	274	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	275	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	276	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	277	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	278	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	279	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	280	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	281	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	282	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	283	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	284	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	285	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	286	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	287	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	288	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	289	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	290	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	291	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	292	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG	257	Db	293	GATCGGCCTCTGGGAGGGTATCATCGCAGCCAAGCAAGCTCATAGGTGATCG</

Db 558 CAGAACGATCACGGCAGATATGCTATTGCAGCTTGACGAAATGGAAGGTAAGTTG 61.7  
 Qy 2788 ATTAATGGATCGCTCAGGATTCTATCCATGGGCCAACAGGAACAGAAATTCCCC 284.7  
 Db 618 ATTAATGGGATTCGCTCAGGATTCTATCCATGGGCCAACAGGAACAGAAATTCCCC 677  
 Qy 2848 CAAGTTAACGGAGCCGTTGACGGATTGAAAGGTACATCGTCTGGGATGTATTAG 2904  
 Db 678 CAAGTTAACGGAGCCGTTGACGGATTGAAAGGTACATCGTCTGGGATGTATTAG 734  
 RESULT 10  
 AAT42917  
 ID AAT42917 standard; DNA; 709 BP.  
 XX  
 AC AAT42917;  
 DT 18-JAN-1997 (first entry)  
 DE SAG12-1 promoter from senescence-associated gene.  
 XX  
 KW SAG12-1; promoter; senescence-associated gene; development;  
 Arabidopsis thaliana; gene regulation; 5'-untranslated region;  
 KW cytokinin biosynthesis; isopentenyltransferase; transgenic plant;  
 KW flowering; seed; fruit; crop improvement; ds.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 FH Key Location/Qualifiers  
 FT promoter 1..602  
 FT /\*tag= a  
 FT 603..709  
 FT /\*tag= b  
 PN WO9629858-A1.  
 XX  
 PD 03-OCT-1996.  
 XX  
 PF 20-FEB-1996; 96WO-US002313.  
 XX  
 PR 29-MAR-1995; 95US-00413135.  
 XX  
 PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
 XX  
 PI Amasino RM, Gan S;  
 XX  
 DR NPI; 1996-454877/45.  
 XX  
 PT Senescence associated gene promoters, SAG12 and SAG13, - useful for  
 producing genetic constructs for producing transgenic plants having  
 delayed senescence.  
 XX  
 PS Claim 2; Page 28; 38pp; English.  
 XX  
 CC The sequence represents a truncated version of the SAG12-1 promoter  
 (AAT42919) from an Arabidopsis thaliana senescence-associated gene. The  
 sequence also contains part of the SAG12-1 gene 5'-untranslated region.  
 CC The sequence has all regulatory signals required for senescence-specific  
 gene expression, and may be operably linked to a cytokinin biosynthesis  
 CC isopentenyltransferase gene in a vector for expression in a transgenic  
 CC plant. The resulting transgenic plant shows delayed senescence, and shows  
 XX longer vegetative growth, producing more flowers, seeds or fruit.  
 SQ Sequence 709 BP; 279 A; 110 C; 86 G; 234 T; 0 U; 0 Other;  
 Query Match 22.3%; Score 709; DB 2; Length 709;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-110;  
 Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1472 AACGTTAACGGAGATGGTCTCTGGAATAACAGAATCTTGAACCT 1531  
 Db 1 AAGCTTTAACGGATGGTCTCTGGAATAACAGAATCTTGAACCT 60  
 Qy 1532 ATTGATTAGTGAAGACAAAGAAGATTCTGTTTATGTGATTAGTGTGAT 1591  
 Db 61 ATTTGATTAGTGAAGACAAAGAAGATTCTGTTTATGTGATTAGTGTGAT 120  
 Qy 1592 GCATGAAGGTACTACGTACTACAAGAAAATAACATGTACGTAACAGTATCAGCA 1651  
 Db 121 GCATGAAGGTACTACGTACTACAAGAAAATAACATGTACGTAACAGTATCAGCA 180  
 Qy 1652 TGTAAGTATTTCACAAATAATTACTCATGATAGATTTTTGAATG 1711  
 Db 181 TGTAAGTATTTCACAAATAATTACTCATGATAGATTTTTGAATG 240  
 Qy 1712 TCAATTAAATGTTCTTAATTTAATTAAATTAAGGAATATTA 1771  
 Db 241 TCAATTAAATGCTTCTTAATTTAATTAAATTAAGGAATATTA 300  
 Qy 1772 TGCACAAACATCATCAACACATCAACTTCATCAATTAAATGTACACAGTAGGAA 1831  
 Db 361 AATAAATTACTAGATAACAATTCTTAATCATCAATTAAATTAAGGAATATTA 420  
 Qy 1892 TAACCCACCACTAAATTACTAAATCCGAGCAAAGTGAGTGAACAGACTGATT 1951  
 Db 421 TAACCCACCACTAAATTACTAAATCCGAGCAAAGTGAGTGAACAGACTGATT 480  
 Qy 1952 CAGGTGATGTTAGACTAAATGGCTACGTATCAAACATCAACGATCATTTAGTTA 2011  
 Db 481 CAGGTGATGTTAGACTAAATGGCTACGTATCAAACATCAACGATCATTTAGTTA 540  
 Qy 2012 TGAATGTAATGTCATTACTGTAAACAAATGCTTGTGATTCATCACTCA 2071  
 Db 541 TGAATGTAATGTCATTACTGTAAACAAATGCTTGTGATTCATCACTCA 600  
 Qy 2072 TGTGAACATTGAAATTACATCAACCTTCACTATAAACCCATCTCAGTACCT 2131  
 Db 601 TGTGAACATTGAAATTACATCAACCTTCACTATAAACCCATCTCAGTACCT 660  
 Qy 2132 TCTGAAGTAATCAAATTAGGCAAAAGTCATTAATTCTCCTAAACC 2180  
 Db 661 TCTGAAGTAATCAAATTAGGCAAAAGTCATTAATTCTCCTAAACC 709  
 RESULT 11  
 AAD33337  
 ID AAD33337 standard; DNA; 709 BP.  
 XX  
 AC AAD33337;  
 DT 01-JUL-2002 (first entry)  
 XX  
 DE Arabidopsis thaliana truncated SAG12 promoter.  
 XX  
 KW Senescence associated gene; SAG-12; transgenic plant; transgenic;  
 KW senescence-specific promoter; senescence characteristic; ds.  
 OS Arabidopsis thaliana.  
 XX  
 FH Key Location/Qualifiers  
 FT promoter 1..604  
 FT /\*tag= a  
 FT /\*note= "SAG12 promoter fragment"  
 FT 5'UTR 605..709  
 FT /\*tag= b  
 XX  
 PN US6359197-B1.  
 XX  
 PD 19-MAR-2002.  
 XX  
 PP 17-NOV-1997; 97US-00971395.

PR	29-MAR-1995;	95US-00413135.	Db	541 TGAATGAGTCACTTGAAACAAATGCTTGATTGGATCAATCACCCTA
XX	(WISC ) WISCONSIN ALUMNI RES FOUND.		QY	2072 TGTGAACATTAGCAATTACATCACCTTCACTATAACCCATCTCAGTACCT
PA			Db	601 TGTGAACATTAGCAATTACATCACCTTCACTATAACCCATCTCAGTACCT
XX			QY	2132 TCTGAAGTAATCAATTAAAGAGCAAAGTCATTAACTTCTAAACC 709
PI	Amasino RM, Gan S, Noh Y;		Db	661 TCTGAAGTAATCAATTAAAGAGCAAAGTCATTAACTTCTAAACC 709
XX	DR	WPI; 2002-291012/33.	QY	
PT	Novel senescence associated promoter sequence connected to a protein-altered senescence characteristics.		Db	
XX	PS	Example; Col 17-20; 21pp; English.	QY	
XX	CC	The invention relates to a genetic construct comprising senescence specific promoter, preferably senescence associated gene (SAG)-12	Db	
CC	CC	promoter operably connected to a protein-coding DNA sequence not natively connected to the promoter. The senescence associated promoters are useful for the creation of transgenic plants with altered senescence characteristics. Genetic constructs can be inserted into plants which become effective only upon plant cells entering senescence. For example, a gene encoding a biosynthetic enzyme under the control of a senescence specific promoter can be inserted into a plant, without having the tissues of the plant exposed to the excess of cytokinin during pre-senescence growth. Then at the onset of senescence, the senescence-specific promoter activates cytokinin production to alter the progression of senescence in the plant. The present sequence is <i>Arabidopsis thaliana</i> truncated SAG12 promoter	QY	
XX	SQ	Sequence 709 BP; 279 A; 110 C; 86 G; 234 T; 0 U; 0 Other;	Db	
Query Match	22.3%	Score 709; DB 6; Length 709;	QY	RESULT 12
Best Local Similarity	100.0%	Pred. No. 5.2e-110;	ID	AAN70790
Matches	709;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ID	AAN70790 standard; DNA; 723 BP.
QY	1472 AAGCTTTAACCTGCACGAATGGTCTCTGTGAATAACAGAACTTGAAATTCAACT	1531	XX	AC
Db	1 AAGCTTTAACCTGCACGAATGGTCTCTGTGAATAACAGAACTTGAAATTCAACT	60	XX	AC
QY	1532 ATTTGATTAGTGAAGACAAAAGAAGATTCCTGTTTATGTGATTGATTGAT	1591	DT	25-MAR-2003 (revised)
Db	61 ATTTGATTAGTGAAGACAAAAGAAGATTCCTGTTTATGTGATTGATTGAT	120	DT	03-OCT-2002 (revised)
QY	1592 GCATGAAAGGTACCTACGTAACAGAAATAACATGTACGTAACTACGTATCAGCA	1651	XX	19-MAR-1991 (first entry)
Db	121 GCATGAAAGGTACCTACGTAACAGAAATAACATGTACGTAACTACGTATCAGCA	130	DE	Sequence of tmr gene found in the Eco RI fragment of the Agrobacterium tumefaciens Ti plasmid.
QY	1652 TGTAAAGTATTTCACAATAATTATAATTAAATTAAAGGAATATTTA 1711		DE	DE
Db	181 TGTAAAGTATTTCACAATAATTATAATTAAAGGAATATTTA 240		XX	KW
QY	1712 TCAATTAAATGCTTTCTTAATTAATTAAATTAAAGGAATATTTA 1771		XX	Cytokin biosynthetic enzyme; trans-zeatin; phytohormone; ss.
Db	241 TCAATTAAATGCTTTCTTAATTAATTAAATTAAAGGAATATTTA 300		XX	OS
QY	1772 TGCAAAACATCATCAACACATATCCAACCTCGAAATCTCTATAGTACACAAGTAGAGAA	1831	XX	OS
Db	301 TGCAAAACATCATCAACACATATCCAACCTCGAAATCTCTATAGTACACAAGTAGAGAA	360	XX	FH
QY	1832 AATAAATTACTAGATACAACACTCTTAATCATCAATTATAATTAGAAACTAAT	1891	FT	FT
Db	361 AATAAATTACTAGATACAACACTCTTAATCATCAATTATAATTAGAAACTAAT	420	PN	FT
QY	1892 TAAACCCACCAATTAACTAAATCCGAGCAAGTGAGTGAACAGACTGATT	1951	XX	FT
Db	421 TAAACCCACCAATTAACTAAATCCGAGCAAGTGAGTGAACAGACTGATT	480	PD	FT
QY	1952 CAGGTTGATGAGTAAATGGCTACGTATCAAACATCAACGATCATTAGTTATGTA	2011	XX	AU8770154-A.
Db	481 CAGGTTGATGAGTAAATGGCTACGTATCAAACATCAACGATCATTAGTTATGTA	540	XX	24-SEP-1987.
QY	2012 TGAATGAGTCACTTGAAACAAATGCTTGATTGGATCAATCACCCTA	2071	XX	18-MAR-1987; 87AU-00070154.
QY			XX	19-MAR-1986; 86US-00841464.
QY			XX	11-APR-1986; 86US-00850963.
QY			XX	(UVOR-) UNIV OREGON STATE.
QY			XX	Morris RO, Regier DA;
Db			XX	DR
QY			XX	WPI; 1987-313994/45.
Db			XX	P-PSDB; AAP70484.
QY			XX	New recombinant DNA molecules - for prodn. of cytokinin(s) in good yields by cultivating Escherichia coli transformants.
Db			XX	Example; Fig 5; 59pp; English.
QY			XX	tmr is a designation for a gene which codes for a cytokinin biosynthetic enzyme and which can be found in the ECOI fragment of the Agrobacterium tumefaciens Ti plasmid. tzs is a designation for a gene which codes for a cytokinin biosynthetic enzyme and which can be found in or near the vir region of the Agrobacterium tumefaciens Ti plasmid pTrc58. ptz is a designation for a gene which codes for a cytokinin biosynthetic enzyme and which can be found in the larger (105 kb) plasmid of <i>P. savastanoi</i> strain 1006. When tmr and tzs are included in the same plasmid, there is a good increase in trans-zeatin yield. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)
QY			XX	Sequence 723 BP; 191 A; 175 C; 186 G; 171 T; 0 U; 0 Other;
QY			XX	Query Match 22.0%; Score 701.2; DB 1; Length 723;
QY			XX	Best Local Similarity 99.4%; Pred. No. 1.1e-108; Mismatches 3; Indels 1; Gaps 1;
Db			XX	Matches 714; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY			XX	2188 CTGCATCTAATTCTGGTCAACTTGACAGG-AAAGACGACGGGATAGCTCTG 2246

Db	6	CTGCATCTAATTTCGGTCCAACTTGCACAGGAAGAACGACCGACGGATAGCTCTGC	65	XX		
QY	2247	CCAGGCAGACAGGGCTCCAGTCTTTCGCTTGATCGGTCAATCGTCTCTCAACTAC	2306	PA	(KENT ) UNIV KENTUCKY RES FOUND.	
Db	66	CCAGCAGACAGGGCTCCAGTCTTTCGCTTGATCGGTCAATCGTCTCTCAACTAC	125	XX		
QY	2307	AACGGAAGGGACGACAAACAGTGGAAAGAACTGAAGAGAACGGCGCTCTACCTGA	2366	PI	Gan S, Xie M, He Y;	
Db	126	AACCGGAAGGGACGACAAACAGTGGAAAGAACTGAAGAGAACGGCGCTCTACCTGA	185	XX	WPI; 2002-442888/47.	
QY	2367	TGATCGGCCTCTGGGGAGGTATCATCGCAGCCAAGCAAGCTCATCATAGGTGATCGA	2426	XX	Bi-directional promoter with common promoter linked in opposite orientation to minimal promoter, useful to direct expression of polynucleotide which confers agronomically significant trait to transgenic plant.	
Db	186	TGATCGGCCTCTGGGGAGGTATCATCGCAGCCAAGCAAGCTCATCATAGGTGATCGA	245	PS		
QY	2427	GGAGGTGTATAATCATGAGGCCAACGGGGTTATTCTTGAGGGATCCACCTCGTT	2486	XX		
Db	246	GGAGGTGTATAATCATGAGGCCAACGGGGTTATTCTTGAGGGATCCACCTCGTT	305	CC		
QY	2487	GCTCAACTGCATGGCGCAAACAGCTATTGGAGTCAGATTTCGTTGGCATATTATCG	2546	CC		
Db	306	GCTCAACTGCATGGCGCAAACAGCTATTGGAGTCAGATTTCGTTGGCATATTATCG	365	CC		
QY	2547	CCACAAGTTACCGACCAAGAGACCTTCATGAAGGGCCAGGCCAGAGTAAAGCAT	2606	CC		
Db	366	CCACAAGTTACCGACCAAGAGACCTTCATGAAGGGCCAGGCCAGAGTAAAGCAT	425	CC		
QY	2607	GTGACACCCGGCTGCAGGCCATTCTTCAAGAGTGGTTATCTTGGATGAACC	2666	XX		
Db	426	GTGACACCCGGCTGCAGGCCATTCTTCAAGAGTGGTTATCTTGGATGAACC	485	SQ		
QY	2667	TGGGCTGAGGCCATTCTGAAAGAGATCGATGATCGATGAGATCGCTTAGTGTGCTAG	2726	Sequence	613 BP; 241 A; 100 C; 64 G; 208 T; 0 U; 0 Other;	
Db	486	TGGGCTGAGGCCATTCTGAAAGAGATCGATGATCGATGAGATCGCTTAGTGTGCTAG	545	Query Match.	17.9%; Score 569.4; DB 6; Length 613;	
QY	2727	CCAGAACCGAGATCACGGCAGATATGCTATGCGCTGACGCAAATATGGAAGGTAAGT	2786	Best Local Similarity	99.8%; Pred No. 1.4e-86;	
Db	546	CCAGAACCGAGATCACGGCAGATATGCTATGCGCTGACGCAAATATGGAAGGTAAGT	605	Matches	570; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2787	GATTAATGGGATCGCTAGGATTTCATCCATGGGCCAACAGGAACAGAAATTCCC	2846	Db	1604 CCTTACGTACTACAGAAATAACATGTACGTACTACGTATCAGCATGTAAGATT	1663
Db	606	GATTAATGGGATCGCTAGGATTTCATCCATGGGCCAACAGGAACAGAAATTCCC	665	QY	1664 TTTTCCAATAATTATACTCATGATAGTTTTGAATGTCAATTAAAT	1723
QY	2847	CCAAAGTTAACCGAGCCGTTTCGACGGATTGAAAGTCATCCGTTGGAATGTATTAG	2904	Db	65 TTTCAGTAAATAATTATACTCATGATAGTTTTGAATGTCAATTAAAT	124
Db	666	CCAAAGTTAACCGAGCCGTTTCGACGGATTGAAAGTCATCCGTTGGAATGTATTAG	723	QY	1724 GCTTCTTAATAATTATACTCATGATAGTTTTGAATGTCAATTAAAT	1783
RESULT 13				Db	125 GCTTCTTAATAATTATACTCATGATAGTTTTGAATGTCAATTAAAT	184
AAD44425				QY	1784 TCAACACATATCCAACTTCAAATCTCTATAGTACAAGTAGAGAAATAATTAC	1843
ID AAD44425 standard; DNA; 613 BP.				Db	185 TCAACACATATCCAACTTCAAATCTCTATAGTACAAGTAGAGAAATAATTAC	244
XX				QY	1844 TAGATACAACTTCAAATTATACTCATGAGTGTGAAAGACTTGTGAGTTGATGTA	1903
AC				Db	245 TAGATACAACTTCAAATTATACTCATGAGTGTGAAAGACTTGTGAGTTGATGTA	304
XX				QY	1904 TAAATTAACCAAATCCGACAAAGTGTGAAAGACTTGTGAGTTGATGTA	1963
DE				Db	305 TAAATTAACCAAATCCGACAAAGTGTGAAAGACTTGTGAGTTGATGTA	304
XX				QY	1964 GGACTAAATGGCTACGTTCAAACATCAACGATCATTTAGTTAGTGTGAGTTGATGTA	2023
KW				Db	365 GGACTAAATGGCTACGTTCAAACATCAACGATCATTTAGTTAGTGTGAGTTGATGTA	424
KW				QY	2024 GTCTTACGTTCAAACAAATGCTTGTGATTCAGTCAATCTCATGTGAACTTAG	2083
KW				Db	425 GTCTTACGTTCAAACAAATGCTTGTGATTCAGTCAATCTCATGTGAACTTAG	484
XX				QY	2084 CAATACATCAACCTTATTTCACATAAAACCCATCTCACTACCTCATGTGAACTTAG	2143
OS				Db	485 CAATACATCAACCTTATTTCACATAAAACCCATCTCACTACCTCATGTGAACTTAG	544
XX				QY	2144 AAATTAAGGAAAGTCATTAACTTCTCCT	2174
PN				Db	545 AAATTAAGGAAAGTCATTAACTTCTCCT	575
XX						
PD						
XX						
PF						
XX						
PR						
07-APR-2000; 2000US-00545244.						
07-APR-2000; 2000US-00545244.						



PT having enhanced levels of cytokinin expression, improved stress tolerance  
 PT and yield stability.  
 XX

PS Disclosure; Page 16; 76pp; English.

CC The present sequence represents an isopentenyl transferase gene fragment.  
 CC The fragment was used to produce the recombinant DNA molecules of the  
 CC invention. These comprise a genetic construct consisting of a promoter  
 CC directing temporal and/or spatial gene expression in plant seed  
 CC operatively linked to a cytokinin modulating gene. The recombinant DNA  
 CC molecules are useful for producing fertile, transgenic plants capable of  
 CC regulated expression of a cytokinin modulating gene in developing seeds.  
 CC They are also useful for improving stress tolerance and yield stability  
 CC in plants. The preferential expression of recombinant DNA molecules of  
 CC the invention occurs about 14-25 days after pollination. The transgenic  
 CC plants thus produced have enhanced levels of cytokinin expression exhibit  
 CC improved seed size, decreased tip kernel abortion and increased seed set  
 CC during unfavourable environmental conditions

XX Sequence 721 BP; 182 A; 176 C; 191 G; 172 T; 0 U; 0 Other;

Query Match 16.8%; Score 536; DB 3; Length 721;  
 Best Local Similarity 84.6%; Pred. No. 5.8e-81; Mismatches 110; Indels 0; Gaps 0;  
 Matches 602; Conservative 0;

QY 2188 CTGCATCTAATTTCGGTCCAACCTGCACAGGAAGACGACGACGGCGTAGCTCTTGCC 2247  
 Db 8 CTACGTCTAAATTTCGGTCCAACCTGCACAGGAAGACATCGACTGCGATAGCTCTTGCC 67

QY 2248 CAGCAGACAGGGCTCCAGTCTTCGCTTGATCGGGTCAAATCGTGTCTCAACTATCA 2307  
 Db 68 CAGCAGACTGGCTCCAGTCTCGCTCGATCGCGTCCAAATGCTGTCTCAACTATCA 127

QY 2308 ACCGAAAGGGGACGACCAACAGTGGAGACTGAAGGAACGACGGCTCTACCTTGAT 2367  
 Db 128 ACCGAAAGGGGACCAACAGTGGAGAACTGAAGGAACGACTCGTGTACTTGAT 187

QY 2368 GATGGCCTCTGGTGGAGGGTATCATCGAGCCAAGCAAGCTCATCATAGGCTGAG 2427  
 Db 188 GATGGCCTTGGTAAAGGTATCATTAACGCCAACGCTCATGAGGCTCATGGC 247

QY 2428 GAGGTGTATAATCATGAGGCCAACGGGGCTATCTGAGGGAGATCCACCTCGTG 2487  
 Db 248 GAGGTGCACAAATCAGGAGCCAAGGGGCTATTCTGAGGGAGATCTCGTTG 307

QY 2488 CTCAACTGCTAGGGCGAAACAGCTATTGGAGTGCAGATTTCGTTGCAATTATTCGC 2547  
 Db 308 CTCAGGTGCATGGGCAAAGTCGTTATTGGAAAGCGGGATTTCGTTGCAATTATTCGC 367

QY 2548 CACAAGTTACCGGACCAAGAGACCTTCATGAAAGGCCAACGCCAGAGTTAACGATG 2607  
 Db 368 AACGAGTTAGGAGAGGAGCTCATGAGGTGGCCAAGCCAGAGTTAACGAGATG 427

QY 2608 TTGACCCCCGCTGCAGGCCATTCTTATTCAGAGGTGTTATCTTGGAAATGAAACCT 2667  
 Db 428 TTACGGCCCTCTGCAGGTCTTCTTATTCAGAGGTGTTCAACTTGGAGGGAGCT 487

QY 2668 CGGCTGAGGCCATTCTGAAAGAGATCGATGGATATGCCATGTTGCTAG 2727  
 Db 488 CGCTGAGGCCATACTGGAGGGATCGATGGATATGCCATGCTTGTGCTTGTAC 547

QY 2728 CAGAACAGATCACGGCAGATATGCTATGCGCTTGACCAAATATGAAAGTAAGTTG 2787  
 Db 548 CAGAACAGATCACGCCGATATGCTATGCGCTTGACCAAATATGAAATTCCT 607

QY 2788 ATTAATGGGATCGCTCAGGAGTATTTCATCCATGGCCACAGGACAGAAATCCCC 2847  
 Db 608 ATTCACGGTATCGCTCAGGAGTTCTAATCCATGGCCACAGGACAGAAATTCCT 667

QY 2848 CAAGTTAACGCCAGCCGTTGACGGATTCGAGGTATCGGTGGATGT 2899  
 Db 668 TTGGTGGCCGACAGCTGTCGAAGCGCTTGTAGGACCACATTTCGAATGT 719

Search completed: June 9, 2004, 23:39:19  
 Job time : 1749 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2004, 22:40:04 ; Search time 249 Seconds  
(without alignments)  
7094.011 Million cell updates/sec

Title: US-10-072-077A-1

Perfect score: 3183

Sequence: 1 gatatctcttttattatcca.....tatgttactagatcgaaattc 3183

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
 5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq:\*
 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	3183	100.0	3183	1 US-08-413-135-1
2	3171	99.6	3182	4 US-08-971-395-1
3	734.8	23.1	745	3 US-09-073-587-4
4	733.4	23.0	24595	6 5428147-1
5	709	22.3	709	1 US-08-413-135-2
6	709	22.3	709	4 US-08-971-395-2
7	569.4	17.9	613	4 US-09-545-244A-11
8	344.4	10.8	584	1 US-08-054-985-2
9	257.2	8.1	1829	1 US-07-966-187-17
10	257.2	8.1	1863	1 US-08-525-507-16
11	257.2	8.1	1863	2 US-08-475-427-9
12	257.2	8.1	1863	2 US-07-842-165-9
13	257.2	8.1	4284	1 US-08-525-507-14
14	256.2	8.0	15397	2 US-08-673-768-1
15	256.2	8.0	15397	2 US-08-673-768-1
16	256	8.0	2633	1 US-08-452-267-2
17	256	8.0	2633	3 US-09-123-644-2
18	256	8.0	534	1 US-08-452-267-3
19	256	8.0	534	3 US-09-123-644-3
20	255	8.0	6548	3 US-08-894-440-1
21	255	8.0	6548	3 US-08-817-188-2
22	255	8.0	6548	4 US-09-458-093-1
23	254.2	8.0	2709	4 US-09-319-275A-12
24	253.2	8.0	9299	4 US-09-097-319A-19
25	253.2	8.0	9335	4 US-09-097-319A-19
26	253.2	8.0	10160	4 US-09-097-319A-8
27	253.2	8.0	11784	4 US-09-097-319A-9

RESULT 1  
US-08-413-135-1

Sequence 1, Application US/08413135

Patent No. 5689042

GENERAL INFORMATION:

APPLICANT: Amasino, Richard M.

APPLICANT: Gan, Sushang

TITLE OF INVENTION: Transgenic Plants with Altered Senescence Characteristics

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53703

ALIGMENTS

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER: IBM PC compatible

APPLICATION NUMBER: US/08/413,135

CURRENT APPLICATION DATA:

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 960296.92808

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3183 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "SAG12-1 Promoter DNA"

US-08-413-135-1

Query Match 100.0%; Score 3183; DB 1; Length 3183;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATATCCTTTTATTCAGAACATAAGTTGAGATATGTTGAGAAGAGGACAATT 60

Db 1 GATATCCTTTTATTCAGAACATAAGTTGAGATATGTTGAGAAGAGGACAATT 60

QY	61	CTCGGGAGCACCGAGTCGTTTATAGAAACCGATTGTATTGACTGAGC	120	QY	1141	TTACACTCAGCCAATATGATTGGATTAAGTCAAATGCAATTGTCAGTATCC	1200
Db	61	CTCGGGAGCACCGAGTCGTTTATAGACTGAGC	120	Db	1141	TTACACTCAGCCAATATGATTGGATTAAGTCAAATGCAATTGTCAGTATCC	1200
QY	121	AAAAAGTAATCGTGATGTAAATTAAATTAAATTAAATTAAATTAAATTAA	180	QY	1201	CTCTGCGCTAATGATTCAATATTCTTATATTCCCTAACATAGAGCTACA	1260
Db	121	AAAAGTAATCGTGATGTAAATTAAATTAAATTAAATTAAATTAAATTAA	180	Db	1201	CTCTGCGCTAATGATTCAATATTCTTATATTCCCTAACATAGAGCTACA	1260
QY	181	AAATGATTAGTATCATAGCTAATAATAGCATGATCTAAATTGTTGACACCTT	240	QY	1261	TTTATATTGTTCTAATGACAGGAAACTTCATAGAGATTGAGATAGTAAATGTT	1320
Db	181	AAATGATTAGTATCATAGCTAATAATAGCATGATCTAAATTGTTGACACCTT	240	Db	1261	TTTATATTGTTCTAATGACAGGAAACTTCATAGAGATTGAGATAGTAAATGTT	1320
QY	241	TTTCTCTTGGTTTACATAGAGAACCTAACATGTACGTTCAATT	300	QY	1321	GGGAACATCATGGACAGGAACCTTCATAGAGATTGAGATAGTAAATGTT	1380
Db	241	TTTCTCTTGGTTTACATAGAGAACCTAACATGTACGTTCAATT	300	Db	1321	GGGAACATCATGGACAGGAACCTTCATAGAGATTGAGATAGTAAATGTT	1380
QY	301	AATTAAACATATTCCAACTTACATTAGAGAACCTAACATGTACGTTCAATT	360	QY	1381	ACTTACCGTAATGAGACTTCACTGTTTGTGAGATGACTATGATCAATT	1380
Db	301	AATTAAACATATTCCAACTTACATTAGAGAACCTAACATGTACGTTCAATT	360	Db	1381	ACTTACCGTAATGAGACTTCACTGTTTGTGAGATGACTATGATCAATT	1380
QY	361	GAATAGTTGATATGAAATTGTTAGATCAACTCAATATGATCAATGATGATAT	420	QY	1441	TGTGAAATACAGAACTTGTGAAATTGATCAACTTACAGGAAATTAACCTACAAAGAAT	1440
Db	361	GAATAGTTGATATGAAATTGTTAGATCAACTCAATATGATCAATGATGATAT	420	Db	1441	TGTGAAATACAGAACTTGTGAAATTGATCAACTTACAGGAAATTAACCTACAAAGAAT	1440
QY	421	ATGAACTCAGTGTATACAAGAAATTGCTATTAAATACCGATCATGAGTGT	480	QY	1501	TGTGAAATACAGAACTTGTGAAATTGATCAACTTACAGGAAATTAACCTACAAAGAAT	1500
Db	421	ATGAACTCAGTGTATACAAGAAATTGCTATTAAATACCGATCATGAGTGT	480	Db	1501	TGTGAAATACAGAACTTGTGAAATTGATCAACTTACAGGAAATTAACCTACAAAGAAT	1500
QY	481	AAAAGTGTCAAATATGACATGAAAGCGTTTGCCTACCGGATAGGTT	540	QY	1561	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGTTCT	1560
Db	481	AAAAGTGTCAAATATGACATGAAAGCGTTTGCCTACCGGATAGGTT	540	Db	1561	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGTTCT	1560
QY	541	GGAACTCTCAAATAATTGGCCATTAGTATTTGGCTTAAGGCTTACGGTA	600	QY	1641	TGTGAAATACAGAACTTGTGAAATTGATCAACTTACAGGAAATTAACCTACAAAGAAT	1640
Db	541	GGAACTCTCAAATAATTGGCCATTAGTATTTGGCTTAAGGCTTACGGTA	600	Db	1641	TGTGAAATACAGAACTTGTGAAATTGATCAACTTACAGGAAATTAACCTACAAAGAAT	1640
QY	601	GAGACGAGGAAGAAGATGGTCAGTAACAAACAGAGACACTCGTATTGTTGTA	660	QY	1651	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
Db	601	GAGACGAGGAAGAAGATGGTCAGTAACAAACAGAGACACTCGTATTGTTGTA	660	Db	1651	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
QY	661	CTTGGTAGCACTCGATTTGCCAGTAACAAACTGACAACCTCGTA	720	QY	1661	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
Db	661	CTTGGTAGCACTCGATTTGCCAGTAACAAACTGACAACCTCGTA	720	Db	1661	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
QY	721	TCGTTATTAGTTGTACTGGTACCTTGGTAAGAAAGTGTATAGTTAACCTG	780	QY	1671	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
Db	721	TCGTTATTAGTTGTACTGGTACCTTGGTAAGAAAGTGTATAGTTAACCTG	780	Db	1671	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
QY	781	TGTGTCTAGGGTATTGTTGACTAGGGGATTCTCACATCACAA	840	QY	1681	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
Db	781	TGTGTCTAGGGTATTGTTGACTAGGGGATTCTCACATCACAA	840	Db	1681	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
QY	841	TAACAAGTTTATAGTTTAACTTACATCACAA	900	QY	1691	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
Db	841	TAACAAGTTTATAGTTTAACTTACATCACAA	900	Db	1691	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
QY	901	TTRACACCGATTTCCTGTACAGAAATTCAATTACCGTT	960	QY	1701	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
Db	901	TTRACACCGATTTCCTGTACAGAAATTCAATTACCGTT	960	Db	1701	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
QY	961	GACATTATAAGTTAACGTTTACAATTAAATTACCATGTAAGTCCAGT	1020	QY	1711	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
Db	961	GACATTATAAGTTAACGTTTACAATTAAATTACCATGTAAGTCCAGT	1020	Db	1711	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
QY	1021	TATGTCTACTTCTTGTAAAGAAACTAACTTACATGTAAGTCCAGT	1080	QY	1721	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
Db	1021	TATGTCTACTTCTTGTAAAGAAACTAACTTACATGTAAGTCCAGT	1080	Db	1721	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
QY	1081	ATCATTATAATTGAAATATGCAATTGTTGAAATTGTTAGACGG	1140	QY	1731	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
Db	1081	ATCATTATAATTGAAATATGCAATTGTTGAAATTGTTAGACGG	1140	Db	1731	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620
QY	2221	AAGACGACGGCGATAGCTCTGCCAGCAGACAGGGCTCCAGCCTTCGCTGAT	2280	QY	1741	TCCTGTTTATGTTGATTGATTCAAACTATTGATGAAAGTACCTACGTACAGGAA	1620

APPLICANT: Amasino, Richard M  
 APPLICANT: No. 6359197, Yoo-Sun  
 TITLE OF INVENTION: Transgenic Plants with Altered  
 TITLE OF INVENTION: Senescence Characteristics  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Quarles & Brady  
 STREET: 1 South Pinckney Street  
 CITY: Madison  
 STATE: WI  
 COUNTRY: US  
 ZIP: 53701-2113  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/971, 395  
 FILING DATE:  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seay, Nicholas J.  
 REGISTRATION NUMBER: 27386  
 REFERENCE/DOCKET NUMBER: 960296.94908  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 608-251-5000  
 TELEFAX: 608-251-9166  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3182 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-971-395-1

Query Match 99.6%; Score 3171; DB 4; Length 3182;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3182; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 Query 1 GATATCTCTTTATATTCAAACAAATAAGTTGAGATATGTTGAGAAGAGGACAACATT 60  
 Db 1 GATATCTCTTTATATTCAAACAAATAAGTTGAGATATGTTGAGAAGAGGACAACATT 60  
 Query 61 CTCTGGAGCACCGAGCTGTGTTTATATTAGAAACCCGATTGTTATTTAGACTGAGAC 120  
 Db 61 CTCTGGAGCACCGAGCTGTGTTTATATTAGAAACCCGATTGTTATTTAGACTGAGAC 120  
 Query 121 AAAAAGTAATCAGTTAATAGCATGATAATAAACATGTTAATTTAACATTAGTTCATCACGTTTCGATAAA 180  
 Db 121 AAAAAGTAATCAGTTAATAGCATGATAATAAACATGTTAATTTAACATTAGTTCATCACGTTTCGATAAA 180  
 Query 181 AAATGATTAGTTATCAGTTAATAGCATGATAATAAACATGTTAATTTAACATTAGTTCATCACGTTTCGATAAA 240  
 Db 181 AAATGATTAGTTATCAGTTAATAGCATGATAATAAACATGTTAATTTAACATTAGTTCATCACGTTTCGATAAA 240  
 Query 241 TTTCTCTCTTGGTTCTTAACATAGAAAGCCATAACATGTTACGTTCAATT 300  
 Db 241 TTTCTCTCTTGGTTCTTAACATAGAAAGCCATAACATGTTACGTTCAATT 300  
 Query 301 AATTAACAAATATTCCAAGTTTATACATGTTAATTTAACATTAGTTCATCACGTTTCGATAAA 360  
 Db 301 AATTAACAAATATTCCAAGTTTATACATGTTAATTTAACATTAGTTCATCACGTTTCGATAAA 360  
 Query 361 GAATAGTTGATTAGTCAACTCAATAATGATCAATGATGTTATATGATCAATGATGTTATAT 420  
 Db 361 GAATAGTTGATTAGTCAACTCAATAATGATCAATGATGTTATATGATCAATGATGTTATAT 420  
 Query 421 ATGAACCTCAGTTGTTACAAGAAATGCTTAAATACCGATCATGAAGTGT 480  
 Db 421 ATGAACCTCAGTTGTTACAAGAAATGCTTAAATACCGATCATGAAGTGT 480  
 ; GENERAL INFORMATION:  
 RESULT 2

US-08-971-395-1  
 ; Sequence 1, Application US/08971395  
 ; Patient No. 6359197

QY	481	AAAAGTGTCAAGATATGACATGAGCGTTTGCTTACCGGTATCGAGTTAGGTT	540	QY	1561	TCTTGTTTATGTGATTAGTGATGCATAAGGTACTACAAAGAA	1620
Db	481	AAAAGTGTCAAGATATGACATGAGCGTTTGCTTACCGGTATCGAGTTAGGTT	540	Db	1561	TCCTGTTTATGTGATTAGTGATGCATAAGGTACTACAAAGAA	1620
QY	541	GGATCTCTCAAGAATATTGGCCATATTAGTTATTTGGCTTAAGCCTTGGCAA	600	QY	1621	AAATAACATGTCACTACGTATGCATAAGTATTGCTTCCAATAATTAA	1680
Db	541	GGATCTCTCAAGAATATTGGCCATATTAGTTATTTGGCTTAAGCCTTGGCAA	600	Db	1621	AAATAACATGTCACTACGTATGCATAAGTATTGCTTCCAATAATTAA	1680
QY	601	GAGACGGAGAAAGATGGTCAAGTAAACAAACAGAGACACTCGTATTGTTA	660	QY	1681	TACTCATGATAGATTTTTGAAATGTCAATTAAATGCTTCTTAATATAA	1740
Db	601	GAGACGGAGAAAGATGGTCAAGTAAACAAACAGAGACACTCGTATTGTTA	660	Db	1681	TACTCATGATAGATTTTTGAAATGTCAATTAAATGCTTCTTAATATAA	1740
QY	661	CTTGGTAGGCAAGTGGTCAAGTAAACAAACAGAGACACTCGTATTGTTA	720	QY	1741	TTTAATAATAAGGAATATTATGCAAAACATCATCACACATATCCAA	1800
Db	661	CTTGGTAGGCAAGTGGTCAAGTAAACAAACAGAGACACTCGTATTGTTA	720	Db	1741	TTTAATAATAAGGAATATTATGCAAAACATCATCACACATATCCAA	1800
QY	721	TCGTTATTAGTTGTACTGGTACCTTGGTTAGAAAGTGTATAGTTAACAGT	780	QY	1801	TGAAATCTTACAGTAAAGTAAATTGAGAAATAATTACTAGATAAACTCTA	1860
Db	721	TCGTTATTAGTTGTACTGGTACCTTGGTTAGAAAGTGTATAGTTAACAGT	780	Db	1801	TGAAATCTTACAGTAAAGTAAATTGAGAAATAATTACTAGATAAACTCTA	1860
QY	781	TGTGTCATGAGGTGATTGTCAGTTGGTACAGTCAACATCACAA	840	QY	1861	ATCATCAATTAAAGGAATATTATGCAAAACATCATCACACATATCCAA	1920
Db	781	TGTGTCATGAGGTGATTGTCAGTTGGTACAGTCAACATCACAA	840	Db	1861	ATCATCAATTAAAGGAATATTATGCAAAACATCATCACACATATCCAA	1920
QY	841	TAACAAGTTATAGATTTTATAACATTGGCACGCTCGTAAGTTGGTA	900	QY	1921	CCGAGCAAAGTGTAAAGACTTGATTCAAGGTGATGAGGACTAAATTAAC	1980
Db	841	TAACAAGTTATAGATTTTATAACATTGGCACGCTCGTAAGTTGGTA	900	Db	1921	CCGAGCAAAGTGTAAAGACTTGATTCAAGGTGATGAGGACTAAATTAAC	1980
QY	901	TTTACACCGCATTTCCCTGTACAGAAATTCAATTAAACCCACCA	960	QY	1981	TATCAAACATCAACGATCATTAGTTAGTTAGTGTAGTACACTGTAAAC	2040
Db	901	TTTACACCGCATTTCCCTGTACAGAAATTCAATTAAACCCACCA	960	Db	1981	TATCAAACATCAACGATCATTAGTTAGTTAGTGTAGTACACTGTAAAC	2040
QY	961	GACAATTATAAGTTAACGTTTACGTTTACAAATTAAACCCACCA	1020	QY	2041	AAAATGCTTGTGATTCATCACTTCATGTGAAACATTACATCAACCTA	2100
Db	961	GACAATTATAAGTTAACGTTTACGTTTACAAATTAAACCCACCA	1020	Db	2041	AAAATGCTTGTGATTCATCACTTCATGTGAAACATTACATCAACCTA	2100
QY	1021	TATGCTTACTTCTCTGTAGAAACTAACTATACATAAAATTCT	1080	QY	2101	TTTCACTATAAAACCCATCTCGTACCTCTCGTAAAGTAACTAC	2160
Db	1021	TATGCTTACTTCTCTGTAGAAACTAACTATACATAAAATTCT	1080	Db	2101	TTTCACTATAAAACCCATCTCGTACCTCTCGTAAAGTAACTAC	2160
QY	1081	AATCATTATTTGTAATATGCAAGTTTGTAAGAAACTAACTATAC	1140	QY	2161	CATTAACCTCTAAACCATGGACCCCTGCATCTAATTGGTCAAAC	2220
Db	1081	AATCATTATTTGTAATATGCAAGTTTGTAAGAAACTAACTATAC	1140	Db	2161	CATTAACCTCTAAACCATGGAA-CCTGCATCTAATTGGTCAAAC	2219
QY	1141	TTATCACTCAGCCAAATATGATTGTTAGTCCAAATTGTCAGTAC	1200	QY	2221	AAGACGACGCCGATAGCTCTGCCAGCACAGGGCTCCAGTCTCGCTGAT	2280
Db	1141	TTATCACTCAGCCAAATATGATTGTTAGTCCAAATTGTCAGTAC	1200	Db	2220	AAGACGACGCCGATAGCTCTGCCAGCACAGGGCTCCAGTCTCGCTGAT	2279
QY	1201	CTCTTGTCTTAATGATTCTATCCAAATGCAATTGTCAGTAC	1200	QY	2281	CGGGTCAATCGTGTCTCAACTATCACCGGAGCGACGACAACTGGAGACTG	2340
Db	1201	CTCTTGTCTTAATGATTCTATCCAAATGCAATTGTCAGTAC	1200	Db	2280	CGGGTCAATCGTGTCTCAACTATCACCGGAGCGACGACAACTGGAGACTG	2339
QY	1261	TTATATTTGTTCTAATGACAGGAAACTTTAGCAATCATGAAATTG	1260	QY	2341	AAAGGACGACGCCGCTCAACTATCACCGGAGCGACGACAACTGGAGACTG	2400
Db	1261	TTATATTTGTTCTAATGACAGGAAACTTTAGCAATCATGAAATTG	1260	Db	2340	AAAGGACGACGCCGCTCAACTATCACCGGAGCGACGACAACTGGAGACTG	2399
QY	1321	GGAAACATCATTGAACTGGAAACTTTAGCAATCATGAAATTG	1380	QY	2401	AAGCAAGCTCATAGGGCTGATCGAGGGGTATAATCATGAGGCAACGGGGCT	2460
Db	1321	GGAAACATCATTGAACTGGAAACTTTAGCAATCATGAAATTG	1380	Db	2401	AAGCAAGCTCATAGGGCTGATCGAGGGGTATAATCATGAGGCAACGGGGCT	2459
QY	1381	ACTTAGCGTAATGAAGTCACTTGTGTAATGACTATGATTGATCA	1440	QY	2460	ATTCTTGAGGGAGTCACCTCGTGTGATCGCTCTGGAGGTATCATCGAG	2520
Db	1381	ACTTAGCGTAATGAAGTCACTTGTGTAATGACTATGATTGATCA	1440	QY	2521	GCAGATTTCGTGCGATATTTCGCGACAAGTACCCGACCAAGACCTCATGAA	2580
QY	1441	TTGTGAAATCATTTTGTGATTAGCTTAATGAGCTTACCTGCA	1500	QY	2520	GCAGATTTCGTGCGATATTTCGCGACAAGTACCCGACCAAGACCTCATGAA	2579
Db	1441	TTGTGAAATCATTTTGTGATTAGCTTAATGAGCTTACCTGCA	1500	QY	2581	GCGGCCAAGGCCAGAGTTAGCAGATGTTGCCACCCGCTGAGGCCATTCTCATGAA	2640
QY	1501	TGTGAAATACAGAACTTTGTGAAATCAACTATTGATTAGTGA	1560	QY	2580	GCGGCCAAGGCCAGAGTTAGCAGATGTTGCCACCCGCTGAGGCCATTCTCATGAA	2639
Db	1501	TGTGAAATACAGAACTTTGTGAAATCAACTATTGATTAGTGA	1560	QY	2641	GAGTGGTTATTTGAAATGAACTCGCTGGCTGAGGCCATTCTGAAAGAGATCGATGAA	2700

Db 2640 GAGTGTGGTTATCTTGTGGAATGAAACCTCGGCTGAGGCCATTCTGAAGAGATCGATGGA 2699  
 Qy 2701 TATCGATATGCCATGTGTGTTGCTAGCCAGAACAGATCACGGAGATAGCTATTGCAG 2760  
 Db 2700 TATCGATATGCCATGTGTGTTGCTAGCCAGAACAGATCACGGAGATAGCTATTGCAG 2759  
 Qy 2761 CTTGACGCAAATATGGAAGGTAAGTTGATAATGGGATCGCTCAGGATTTCATCCAT 2820  
 Db 2760 CTTGACGCAAATATGGAAGGTAAGTTGATAATGGGATCGCTCAGGATTTCATCCAT 2819  
 Qy 2821 GCGGCCAACAGGAACAGAAATTCCCCAAGTTACGGCAGCCGTTCCACGGATTGAA 2880  
 Db 2820 GCGGCCAACAGGAACAGAAATTCCCCAAGTTACGGCAGCCGTTCCACGGATTGAA 2879  
 Qy 2881 GGTCACTCGGTGGAATGTTAGGTTACGGCAGCCGTTCCACGGATTGAA 2940  
 Db 2880 GGTCACTCGGTGGAATGTTAGGTTACGGCAGCCGTTCCACGGATTGAA 2939  
 Qy 2941 GGCATAAAGTTCTTAAGATGAACTCTGTGCGGCTTGGCATGATATCATATAAT 3000  
 Db 2940 GGCATAAAGTTCTTAAGATGAACTCTGTGCGGCTTGGCATGATATCATATAAT 2999  
 Qy 3001 TTCTGTGAAATTACGTTAACGATGATAATAACATGATGACGTTATTATGA 3060  
 Db 3000 TTCTGTGAAATTACGTTAACGATGATAATAACATGATGACGTTATTATGA 3059  
 Qy 3061 GATGGTTTATGATTAGACTGGGATAATTACATTAATACGGATAGAAAACAAA 3120  
 Db 3060 GATGGTTTATGATTAGACTGGGATAATTACATTAATACGGATAGAAAACAAA 3119  
 Qy 3121 TATGGCGCGAACACTGGGATAATTACATTAATACGGATAGAAAACAAA 3180  
 Db 3120 TATGGCGCGAACACTGGGATAATTACATGGCGCGGTGTCACTATGTTAGATGAA 3179  
 Qy 3181 TTC 3183  
 Db 3180 TTC 3182

RESULT 3  
 US-09-073-587-4  
 Sequence 4, Application US/09073587  
 Patent No. 626852  
 GENERAL INFORMATION:  
 APPLICANT: Li, Yi  
 TITLE OF INVENTION: Transgenic Seedless Plants  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GreenLee, Winner and Sullivan, P.C.  
 STREET: 5370 Manhattan Circle, Suite 201  
 CITY: Boulder  
 STATE: Colorado  
 COUNTRY: US  
 ZIP: 80303  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/073, 587  
 FILING DATE: 06-MAY-1998  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/045, 725  
 FILING DATE: 06-MAY-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ferber, Donna M.  
 REFERENCE/DOCKET NUMBER: 33, 878  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 499-8080  
 RESULT 4

TELEFAX: (303) 499-8089  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 745 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 3..725  
 US-09-073-587-4

Query Match: 23.1%; Score 734.8; DB 3; Length 745;  
 Best Local Similarity 99.7%; Pred. No. 3.2e-151;  
 Matches 736; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Db 8 CCTGCATCTAATTTCGGTCCACTGACAGGAATTCGGTCTTCAGCTCTGC 2246  
 Qy 2247 CCAGCAGACAGGGCTTCCAGTCTTCGGTCTTCAGCTCTGC 67  
 Db 68 CCAGCAGACAGGGCTTCCAGTCTTCGGTCTTCAGCTCTGC 127  
 Qy 2307 AACCGGAAGGGACGACAGTGGAACTGAAAGGAACGACGCGCTCTACCTGA 2366  
 Db 128 AACCGGAAGGGACGACAGTGGAACTGAAAGGAACGACGCGCTCTACCTGA 187  
 Qy 2367 TGATCGGCCTCTGGGGAGGTATCATCGCAGCCAAGCTCATAGGCTGATCGA 2426  
 Db 188 TGATCGGCCTCTGGGGAGGTATCATCGCAGCCAAGCTCATAGGCTGATCGA 247  
 Qy 2427 GGAGGTATAATCATGAGGCCAACGGGGTATCTTGAGGGAGTCCACCTCGT 2486  
 Db 248 GGAGGTATAATCATGAGGCCAACGGGGTATCTTGAGGGAGTCCACCTCGT 307  
 Qy 2487 GCTCAACTGCATGGCGAACAGCTATTGGACTGCGATTCTGGTCATATTG 2546  
 Db 308 GCTCAACTGCATGGCGAACAGCTATTGGACTGCGATTCTGGTCATATTG 367  
 Qy 2547 CCACAAGTTACCGACCAAGAGACCTTATGAAAGGGCAAGGCCAGAGTTAACGAGAT 2606  
 Db 368 CCACAAGTTACCGACCAAGAGACCTTATGAAAGGGCAAGGCCAGAGTTAACGAGAT 427  
 Qy 2607 GTGGCACCCGGCTCAGGCCATTCTAACAGATGGGTTATCTTGGAA 2666  
 Db 428 GTTGCAcccccGCTCAGGCCATTCTAACAGATGGGTTATCTTGGAA 487  
 Qy 2667 TCGGCTGAGGCCATTCTGAAGAGATGGGATATGCCATGTTGCTAG 2726  
 Db 488 TCGGCTGAGGCCATTCTGAAGAGATGGGATATGCCATGTTGCTAG 547  
 Qy 2727 CCAGAACAGATCACGGCAGATGCTATTGCAAGCAATATGGAAGGTAAGT 2786  
 Db 548 CCAGAACAGATCACGGCAGATGCTATTGCAAGCAATATGGAAGGTAAGT 607  
 Qy 2787 GATTAATGGGATCGCTCAGGGATTTCATCCATGGGCCAACAGGAATATCCC 2846  
 Db 608 GATTAATGGGATCGCTCAGGGATTTCATCCATGGGCCAACAGGAATATCCC 667  
 Qy 2847 CCAAGTTACCGCAGCCGCTTCCACGGATTGAAAGGTCATCCGGTCTGGAAATGTTAGGT 2906  
 Db 668 CCAAGTTACCGCAGCCGCTTCCACGGATTGAAAGGTCATCCGGTCTGGAAATGTTAGGT 727  
 Qy 2907 TACGCCAGCCCTGAGCTC 2924  
 Db 728 TACGCCAGCCCTGAGCTC 745

5428147-1  
; Patent No. 5428147  
; APPLICANT: BARKER, RICHARD F.; KEMP, JOHN D.  
; TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS  
; NUMBER OF SEQUENCES: 17  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/91, 538  
; FILING DATE: 13-JUL-1993  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 869, 216  
; FILING DATE: 13-APR-1992  
; APPLICATION NUMBER: 440, 432  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 553, 786  
; FILING DATE: 19-NOV-1983  
; APPLICATION NUMBER: 741, 034  
; FILING DATE: 06-AUG-1991  
; APPLICATION NUMBER: 144, 775  
; FILING DATE: 20-JAN-1988  
; APPLICATION NUMBER: 485, 614  
; FILING DATE: 15-APR-1983  
; APPLICATION NUMBER: 713, 624  
; FILING DATE: 10-JUN-1991  
; APPLICATION NUMBER: 260, 574  
; FILING DATE: 21-OCT-1988  
; APPLICATION NUMBER: 848, 733  
; FILING DATE: 01-APR-1986  
; APPLICATION NUMBER: 535, 354  
; FILING DATE: 26-SEP-1983  
; SEQ ID NO:1:  
; LENGTH: 24595  
; 5428147-1

Query Match 23.0%; Score 733.4; DB 6; Length 24595;  
Best Local Similarity 96.0%; Pred. No. 1.8e-150;  
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 2139 TAATCAAATTAGAGCAAAAGTCATTAACCTTCTAAACCATGGACCCCTGATCTAAT 2198  
Db 8728 TAATATAAAATCAGTTGTATTCAATACTGCAAACAAACTTATGGACCTGCATCTAAT 8787

QY 2199 TTTCGGTCCAACCTGACACAGGAAGAACGACGACGCCGCGATAAGCTCTGGCCAGCACAGG 2258  
Db 8788 TTTCGGTCCAACTTGACACAGGAAGAACGACGACGCCGCGATAAGCTCTGGCCAGCACAGG 8847

QY 2259 GCTTCCAGTCTTCGCTGTATCGGGTCAAATCGTGTCTCAACTATAACGGGAAGCGG 2318  
Db 8848 GCTTCCAGTCTTCGCTGTATCGGGTCAAATCGTGTCTCAACTATAACGGGAAGCGG 8907

QY 2319 ACGACCAACAGTGAAGAACTGAAAGGAACGACGCGCTCTACCTTGATGATCGGCCTCT 2378  
Db 8908 ACGACCAACAGTGAAGAACTGAAAGGAACGACGCGCTCTACCTTGATGATCGGCCTCT 8967

QY 2379 GGTGGGGGTATCATCGCAGCCAAAGCAAGCTCATAGCTGATCGAGGGGTATAA 2438  
Db 8968 GTGGGGGTATCATCGCAGCCAAAGCAAGCTCATAGCTGATCGAGGGGTATAA 9027

QY 2439 TCATGAGGCCAACGGCGGGCTTATCTTGAGGGAGATCACCTCGTGTCTCAACTGCAT 2498  
Db 9028 TCATGAGGCCAACGGCGGGCTTATCTTGAGGGAGATCACCTCGTGTCTCAACTGCAT 9087

QY 2499 GGCGCGAACAGCTATGGAGTGCAAGTTCTGTCAGATTCACCTCGTGTCTCAACTGCAT 2558  
Db 9088 GGCGCGAACAGCTATGGAGTGCAAGTTCTGTCAGATTCACCTCGTGTCTCAACTGCAT 9147

QY 2559 CGACCAAGAGACCTTCATGAAAGGGCCAAGGCCAGAGTTAACCGAGATGTGCACCCGC 2618  
Db 9148 CGACCAAGAGACCTTCATGAAAGGGCCAAGGCCAGAGTTAACCGAGATGTGCACCCGC 9207

QY 2619 TGCAAGGCCATTCTATTATTCAGAGTGGTTATCTTGAAATGAAACCTCGGCTGAGGCC 2678

Db 9208 TGCAGGCCATTCTATTCAAGAGTGGTTATCTTGAAATGAAACCTCGGCTGAGGCC 9267  
QY 2679 CATTCTGAAAGAGATCGATGGATATCGATATGCCATGTTGTTGCTAGGCCAGAACAGAT 2738  
Db 9268 CATTCTGAAAGAGATCGATGGATATCGATATGCCATGTTGTTGCTAGGCCAGAACAGAT 9327

QY 2739 CACGGAGATATGCTATTGCACTGACGCTGACGCAAATATGGAAGGTAAGTTGATTAATGGGAT 2798  
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QY 2799 CGCTCAGGAGTATTCATCCATGCCATGCCAACAGGACAGAAATTCCCCAGTTAACGC 2858  
Db 9388 CGCTCAGGAGTATTCATCCATGCCATGCCAACAGGACAGAAATTCCCCAGTTAACGC 9447

QY 2859 AGCCGCTTCGACGGATTCGAGGTCTCGAATGTTAGGTTACGCCAGCCCT 2918  
Db 9448 AGCCGCTTCGACGGATTGCACTCCGTTCGGAATGTATTAGGTTACGCCAGCCCT 9507

QY 2919 GAG 2921

Db 9508 GCG 9510

RESULT 5  
US-08-413-135-2  
Sequence 2, Application US/08413135  
; Patent No. 5689042  
; GENERAL INFORMATION:  
; APPLICANT: Amasino, Richard M  
; TITLE OF INVENTION: Transgenic Plants with Altered  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 1 South Pinckney Street  
; CITY: Madison  
; STATE: WI  
; COUNTRY: US  
; ZIP: 53703  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/413, 135  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seay, Nicholas J  
; REGISTRATION NUMBER: 27, 386  
; REFERENCE/DOCKET NUMBER: 960296.92808  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 608-251-5000  
; TELEFAX: 608-251-9166  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 709 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "SAG12-1 Promoter DNA  
; DESCRIPTION: (truncated)"  
; US-08-413-135-2

Query Match 22.3%; Score 709; DB 1; Length 709;  
Best Local Similarity 100.0%; Pred. No. 1.3e-145;  
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1472 AAGCTTTAACTTGCACCGATGGTTCTCTGTGAAATAACGAACTTGAATCAA 1531

Db 1 AAGCTTTAACTGCACCGATGGTCTGTGATAACAGAATCTTGAATTCAA 60  
 QY 1532 ATTGATTAGTAGTGAAGAACAAAGAGATCCTGTTTATGTGATTGTGAT 1591  
 Db 61 ATTGATTAGTAGTGAAGAACAAAGAGATCCTGTTTATGTGATTGTGAT 120  
 QY 1592 GCATGAAAGGTACCTACGTACTACAAGAAAATAACATGTACGTAACTACGTATCAGCA 1651  
 121 GCATGAAAGGTACCTACGTACTACAAGAAAATAACATGTACGTAACTACGTATCAGCA 180  
 QY 1652 TGTAAAGTATTTCCTCAAATAATTATACGTAGATTTTTGAAATG 1711  
 181 TGTAAAGTATTTCCTCAAATAATTATACGTAGATTTTGAAATG 240  
 QY 1712 TCAATTAAAATGCTTCTTAATATTAATTATTAATAAGGAATATTTA 1771  
 241 TCAATTAAAATGCTTCTTAATATTAATTATTAATAAGGAATATTTA 300  
 QY 1772 TGCAAAACATCAACACATATCCAACCTTGAAATCTCTATAGTACAAAGTAGAGAA 1831  
 Db 301 TGCAAAACATCAACACATATCCAACCTTGAAATCTCTATAGTACAAAGTAGAGAA 360  
 QY 1832 ATATAATTACTAGATACAAACTCTTAATCATCAATTAAATGTTACAAACTAT 1891  
 361 ATATAATTACTAGATACAAACTCTTAATCATCAATTAAATGTTACAAACTAT 420  
 Db 361 ATATAATTACTAGATACAAACTCTTAATCATCAATTAAATGTTACAAACTAT 420  
 QY 1892 TAAACCCACCCTAAATTAACAAATCCGAGCAAGTGAGTGAACAGACTTGTATT 1951  
 421 TAAACCCACCCTAAATTAACAAATCCGAGCAAGTGAGTGAACAGACTTGTATT 480  
 QY 1952 CAGGTGATGAGACTAAATGGCTACGTACAAACATCAACGATCATTAGTTGT 2011  
 481 CAGGTGATGAGACTAAATGGCTACGTACAAACATCAACGATCATTAGTTGT 540  
 Db 481 CAGGTGATGAGACTAAATGGCTACGTACAAACATCAACGATCATTAGTTGT 540  
 QY 2012 TGAATGAACTGTCATTCTGTAAACAAATGCTTGTGATTGATCACTTCA 2071  
 541 TGAATGAACTGTCATTCTGTAAACAAATGCTTGTGATTGATCACTTCA 600  
 Db 541 TGAATGAACTGTCATTCTGTAAACAAATGCTTGTGATTGATCACTTCA 600  
 QY 2072 TGTGAACTGCAATTACATCAACCTTATTCTACTATAAACCCATCTCAGTACCT 2131  
 601 TGTGAACTGCAATTACATCAACCTTATTCTACTATAAACCCATCTCAGTACCT 660  
 Db 601 TGTGAACTGCAATTACATCAACCTTATTCTACTATAAACCCATCTCAGTACCT 660  
 QY 2132 TCTGAAAGTAATCAAATTAGGACAAAGTCATTACTTCTAAACC 2180  
 Db 661 TCTGAAAGTAATCAAATTAGGACAAAGTCATTACTTCTAAACC 709  
 RESULT 6  
 US-08-971-395-2  
 ; Sequence 2, Application US/08971395  
 ; Patent No. 6359197  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Amasino, Richard M  
 ; APPLICANT: No. 6359197, Yoo-Sun  
 ; APPLICANT: Gan, Susheng  
 ; TITLE OF INVENTION: Transgenic Plants with Altered  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Quarles & Brady  
 ; STREET: 1 South Pinckney Street  
 ; CITY: Madison  
 ; STATE: WI  
 ; COUNTRY: US  
 ; ZIP: 53701-2113  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/971, 395  
 ; FILING DATE:

CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seay, Nicholas J.  
 REGISTRATION NUMBER: 27386  
 REFERENCE/DOCKET NUMBER: 960296.94908  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 608-251-5000  
 TELEFAX: 608-251-9166  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 709 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-971-395-2  
 Query Match 22.3%; Score 709; DB 4; Length 709;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-145;  
 Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 AAGCTTTAACTGCACCGATGGTCTGTGATAACAGAATCTTGAATTCAA 1531  
 QY 1472 AAGCTTTAACTGCACCGATGGTCTGTGATAACAGAATCTTGAATTCAA 1531  
 Db 1 AAGCTTTAACTGCACCGATGGTCTGTGATAACAGAATCTTGAATTCAA 60  
 QY 1532 ATTGATTAGTAGTGAAGAACAAAGAGATCCTGTTTATGTGATTGTGAT 1591  
 61 ATTGATTAGTAGTGAAGAACAAAGAGATCCTGTTTATGTGATTGTGAT 120  
 Db 61 ATTGATTAGTAGTGAAGAACAAAGAGATCCTGTTTATGTGATTGTGAT 120  
 QY 1592 GCATGAAAGGTACCTACGTACTACAAGAAAATAACATGTACGTAACTACGTATCAGCA 1651  
 Db 121 GCATGAAAGGTACCTACGTACTACAAGAAAATAACATGTACGTAACTACGTATCAGCA 180  
 QY 1652 TGTAAAGTATTTCCTCAAATAATTATTAATAAGGAATATTTA 1771  
 181 TGTAAAGTATTTCCTCAAATAATTATTAATAAGGAATATTTA 300  
 Db 181 TGTAAAGTATTTCCTCAAATAATTATTAATAAGGAATATTTA 300  
 QY 1712 TCAATTAAAATGCTTCTTAATATTATTAATAAGGAATATTTA 1771  
 241 TCAATTAAAATGCTTCTTAATATTATTAATAAGGAATATTTA 1771  
 QY 1772 TGCAAAACATCATCAACACATATCCAACCTTGAAATCTCTATAGTACAAAGTAGAGAA 1831  
 301 TGCAAAACATCATCAACACATATCCAACCTTGAAATCTCTATAGTACAAAGTAGAGAA 360  
 Db 301 TGCAAAACATCATCAACACATATCCAACCTTGAAATCTCTATAGTACAAAGTAGAGAA 360  
 QY 1832 ATATAATTACTAGATACAAACTCTTAATCATCAATTAAATGTTCAAACAT 1891  
 361 ATATAATTACTAGATACAAACTCTTAATCATCAATTAAATGTTCAAACAT 420  
 Db 361 ATATAATTACTAGATACAAACTCTTAATCATCAATTAAATGTTCAAACAT 420  
 QY 1892 TAAACCCACCCTAAATTAACAAATCCGAGCAAGTGAGTGAACAGACTTGTATT 1951  
 421 TAAACCCACCCTAAATTAACAAATCCGAGCAAGTGAGTGAACAGACTTGTATT 480  
 Db 421 TAAACCCACCCTAAATTAACAAATCCGAGCAAGTGAGTGAACAGACTTGTATT 480  
 QY 1952 CAGGTGATGAGACTAAATGGCTACGTACAAACATCAACGATCATTAGTTGT 2011  
 481 CAGGTGATGAGACTAAATGGCTACGTACAAACATCAACGATCATTAGTTGT 540  
 Db 481 CAGGTGATGAGACTAAATGGCTACGTACAAACATCAACGATCATTAGTTGT 540  
 QY 2012 TGTGAACTGCAATTACATCAACCTTATTCTACTATAAACCCATCTCAGTACCT 2131  
 541 TGTGAACTGCAATTACATCAACCTTATTCTACTATAAACCCATCTCAGTACCT 600  
 Db 541 TGTGAACTGCAATTACATCAACCTTATTCTACTATAAACCCATCTCAGTACCT 600  
 QY 2072 TGTGAACTGCAATTACATCAACCTTATTCTACTATAAACCCATCTCAGTACCT 2131  
 601 TGTGAACTGCAATTACATCAACCTTATTCTACTATAAACCCATCTCAGTACCT 660  
 Db 601 TGTGAACTGCAATTACATCAACCTTATTCTACTATAAACCCATCTCAGTACCT 660  
 QY 2132 TCTGAAAGTAATCAAATTAGGACAAAGTCATTACTTCTAAACC 2180  
 Db 661 TCTGAAAGTAATCAAATTAGGACAAAGTCATTACTTCTAAACC 709  
 RESULT 7  
 US-09-545-244A-11  
 ; Sequence 11, Application US/09545244A

Patent No. 6388170  
 GENERAL INFORMATION:  
 APPLICANT: Gan, Susheng  
 Xie, Mingtang  
 APPLICANT: He, Yuehui  
 TITLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto  
 FILE REFERENCE: 050229-0210  
 CURRENT APPLICATION NUMBER: US/09/545,244A  
 CURRENT FILING DATE: 2000-04-07  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 11  
 LENGTH: 613  
 TYPE: DNA  
 ORGANISM: synthetic construct  
 US-09-545-244A-11.

Query Match 17.9%; Score 569.4; DB 4; Length 613;  
 Best Local Similarity 99.8%; Pred. No. 3.5e-115;  
 Matches 570; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1604 CCTTACGTACTACAAGAAAATAACATGTACGTAACTACGTATCAGCATGTAAGTATT 1663  
 Db 5 CTTACGTACTACAAGAAAATAACATGTACGTAACTACGTATCAGCATGTAAGTATT 64

QY 1664 TTTTCCAAATAATTATCTCATGATAGATTTTTTTGAAATGTCAATTAAAT 1723  
 Db 65 TTTTCCAAATAATTATCTCATGATAGATTTTTTTGAAATGTCAATTAAAT 124

QY 1724 GCTTTCCTAAATATTAAATTAAATTAAATAAGGAATAATTATGCAACATCA 1783  
 Db 125 GCTTCTTAATATTAAATTAAATTAAATAAGGAATAATTATGCAACATCA 184

QY 1784 TCAACACATACCAACCTCGAAACTCTCATAGTACACAAGTAGAGAAATAATTAC 1843  
 Db 185 TCAACACATATCCAACTTCGAAATCTCTATAGTACACAAGTAGAGAAATAATTAC 244

QY 1844 TAGATACAAACTCTTAATCATCAATTATAATTGTTTACAACATAATTAAACCCAC 1903  
 Db 245 TAGATACAAACTCTTAATCATCAATTATAATTGTTACAACATAATTAAACCCAC 304

QY 1904 TAAATTAACTAAATCCGAGCAAAGTGAGTGAAACAGACTGTGATTTCAGGTGATGTA 1963  
 Db 305 TAAATTAACTAAATCCGAGCAAAGTGAGTGAAACAGACTGTGATTTCAGGTGATGTA 364

QY 1964 GGACTAAATGGCTACGTATCAAACATCAACGATCATTTAGTTATGTAATGAAATGTA 2023  
 Db 365 GGACTAAATGGCTACGTATCAAACATCAACGATCATTTAGTTATGTAATGAAATGTA 424

QY 2024 GTCTTACTGTAAACAAATGCTTGGATCATCACTTCAGTGGAAACATGGAAACATAG 2083  
 Db 425 GTCTTACTGTAAACAAATGCTTGGATCATCACTTCAGTGGAAACATGGAAACATAG 484

QY 2084 CAATTACATCAACCTTAACTAAACCCATCTAGTACCCCTCTGAAGTAATC 2143  
 Db 485 CAATTACATCAACCTTAACTAAACCCATCTAGTACCCCTCTGAAGTAATC 544

QY 2144 AAATAAGAGGCAAAGTCATTAACCTTCT 2174  
 Db 545 AAATAAGAGGCAAAGTCATTAACCTTCT 575

RESULT 8  
 US-08-054-985-2  
 Sequence 2, Application US/08054985  
 Patent No. 5496732  
 GENERAL INFORMATION:  
 APPLICANT: Smigocki, Ann C  
 APPLICANT: Neal Jr., John W  
 TITLE OF INVENTION: ENHANCED INSECT RESISTANCE IN PLANTS  
 TITLE OF INVENTION: GENETICALLY ENGINEERED WITH A PLANT HORMONE GENE  
 TITLE OF INVENTION: INVOLVED  
 TITLE OF INVENTION: IN CYTOKININ BIOSYNTHESIS

---

NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Janelle S Graeter  
 STREET: Room 411, Building 005, BARC-W  
 CITY: Beltsville  
 STATE: Maryland  
 COUNTRY: United States of America  
 ZIP: 20705  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/054,985  
 FILING DATE: 30-APR-1993  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Graeter, Janelle S  
 REGISTRATION NUMBER: 35024  
 REFERENCE/DOCKET NUMBER: 0175.92  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 504-6629  
 TELEFAX: (301) 504-5060  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 584 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Agrobacterium tumefaciens  
 US-08-054-985-2

Query Match 10.8%; Score 344.4; DB 1; Length 584;  
 Best Local Similarity 80.7%; Pred. No. 3.9e-66;  
 Matches 552; Conservative 0; Mismatches 11; Indels 121; Gaps 8;

QY 2187 CCTGCATCTAATTTGGTCCAACTTGACAGGAAGACGACGCCGCGATAGCTCTTGC 2246  
 Db 6 CCTGCATCTAATTTGGTCCAACTTGACAGGAAGACGACGCCGCGATAGCTCTTGC 65

QY 2247 CCAGCAGACAGGGCTCCAGCCTTGCCTGAPCGGTCAAATCGTGTCTCAACTAC 2306  
 Db 66 CCAGCAGACAGGGCT-----GGTCCATGCTGTCTCAACTAC 105

QY 2307 AACCGGAACGGGACGACAAAGTGGAAACTGAAGGAACGACGCCGCGTCTTACCTG 2366  
 Db 106 AACCGGAACGGGACGACAAAGTGGAAACTGAAGGAACGACGCCGCGTCTTACCTG 160

QY 2367 TGATCGGCCTCTGGGGAGGTATCATCGCAGCCAACTGGAAAGGAACGACGCCGCGTCTTACCTG 2426  
 Db 161 -----GGAGGGTATCATCGCAGCCAACTGGAAAGGAACGACGCCGCGTCTTACCTG 205

QY 2427 GGAGGTGATAATCATGAGGCCAACGGGGCTTATTCTGGAGGGATGCCACCTCGTT 2486  
 Db 206 GGAGGTGATAATCATGAGGCCAACGGGGCTTATTCTGGAGGGATGCCACCTCGTT 245

QY 2487 GCTCACTGCATGGGGCAACAGCTTGGAGTCAGATTTCGTTGGCATATTATTCG 2546  
 Db 246 GCTCACTGCATGGGGCAACAGCTTGGAGTCAGATTTCGTTGGCATATTATTCG 305

QY 2547 CCACAGTTACCGACCAAGAGACCTTCATGAAGGCCAACGCCAGAGTTAAG-CAGA 2605  
 Db 306 CCACAGTTACCGACCAAGAGACCTTCATGAAGGCCAACGCCAGAGTTAAGCCAGA 345

QY 2606 TGTGCACCCCGGCAGGCCATTCTTATTCAAGAGTTGTTATCTTGAATGAAC 2665  
 Db 346 TGTGCACCCCGGCAGGCCATTCTTATTCAAGAGTTGTTATCTTGAATGAAC 400

QY 2666 CTCGCGCTGAGGCCATTCTGAAGAGATCGATGGATATCGATGCCATGTTGTTGCTA 2725  
 Db 401 -----TTCGTAAAGAGATCGATGGATATCGATGCCATGTTGCTA 445  
 QY 2726 GCCAGAACAGATCACGGCAGATATGCTATTGCACTGACCAATATGGAAGGTAAGT 2785  
 Db 446 GCCAGAACAGATCACGGCAGATATGCTATTGCA-----GTAGT 485  
 RESULT 9  
 US-07-966-187-17  
 ; Sequence 17, Application US/07966187  
 ; Patent No. 5477001  
 GENERAL INFORMATION:  
 APPLICANT: SASS, Catherine  
 APPLICANT: LEGUAY, Jean-Jacques  
 APPLICANT: GRISON, Rene  
 APPLICANT: TOPPAN, Alain  
 TITLE OF INVENTION: Recombinant DNA coding for a novel protein having beta 1,3 glucanase activity, bacteria containing this DNA, transformed plant cells and plants.  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FOLEY & LARDNER  
 STREET: King Street Station, Suite 500, 1800 Diagonal  
 CITY: Road, PO Box 299  
 STATE: ALEXANDRIA  
 COUNTRY: VIRGINIA  
 ZIP: 22313-0299  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/966,187  
 FILING DATE: 19930125  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/FR92/00268  
 FILING DATE: 25-MAR-1992  
 TELEPHONE: (703) 836-9300  
 TELEX: 899149  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1829 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 FEATURE: CDS  
 LOCATION: 438..1547  
 NAME/KEY: mat\_peptide  
 LOCATION: 537..1547  
 FEATURE:  
 NAME/KEY: sig\_peptide  
 LOCATION: 438..536  
 US-07-966-187-17  
 Query Match 8.1%; Score 257.2; DB 1; Length 1829;  
 Best Local Similarity 98.9%; Pred. No. 5.6e-47;  
 Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Db 486 TGATTAATGGGATCGCTCAGGAGTATTTCATCCATGGGGCAACAGGAACAGAAATTCC 2845  
 QY 2846 CCCAAAGTTAACCGCAGCCGTTTCG 2869  
 546 CCCAAAGTTAACGCAGGGTCATCCG 569  
 Db 1628 GCGATGATTATCATATAATTCTGTGAATTACGTTAACGATGTTAACATGCAA 1687  
 QY 3042 TGCATGACGTTATTATGAGATGGGTTTATGATAGTAGTCCCGCAATTATACATTAA 3101  
 Db 1688 TGCATGACGTTATTATGAGATGGGTTTATGATAGTAGTCCCGCAATTATACATTAA 1747  
 QY 3102 TACGGCATAGAACAAATATGGCGCGCAAATGGGATAATTATCGCGCGGGTGCA 3161  
 Db 1748 TACGGCATAGAACAAATATGGCGCGCAAATGGGATAATTATCGCGCGGGTGCA 1807  
 QY 3162 TCTATGTTACTAGATCGAATT 3183  
 Db 1808 TCTATGTTACTAGATCGAATT 1829  
 RESULT 10  
 US-08-525-507-16  
 ; Sequence 16, Application US/08525507  
 ; Patent No. 5792932  
 GENERAL INFORMATION:  
 APPLICANT: MARCO, Yves  
 APPLICANT: ROBY, Dominique  
 APPLICANT: SCHNEIDER, Michel  
 APPLICANT: TOPPAN, Alain  
 TITLE OF INVENTION: Plant promoter, microorganisms and plant cells containing a unit for the expression of a protein of interest comprising said promoter.  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DENNISON, MESEROLE, POLLACK & SCHEINER  
 STREET: 612 Crystal Square 4 - 1745 Jefferson Davis Highway  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: USA  
 ZIP: 666  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/525,507  
 FILING DATE:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 683-4109  
 TELEX: 899149  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1829 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 FEATURE: CDS  
 LOCATION: 438..1547  
 NAME/KEY: mat\_peptide  
 LOCATION: 537..1547  
 FEATURE:  
 NAME/KEY: sig\_peptide  
 LOCATION: 438..536  
 US-07-966-187-17  
 Query Match 8.1%; Score 257.2; DB 1; Length 1829;  
 Best Local Similarity 98.9%; Pred. No. 5.6e-47;  
 Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Db 1568 CCCGATCGTTCAAACATTGGCAATAAGTTCTTAAGATGATCCCTGTGCCGGCTT 1627  
 QY 2982 GCGATGATTATCATATAATTCTGTGAATTACGTTAACGATGTTAACATGCAA 3041  
 Db 1628 GCGATGATTATCATATAATTCTGTGAATTACGTTAACGATGTTAACATGCAA 1687  
 QY 3042 TGCATGACGTTATTATGAGATGGGTTTATGATAGTAGTCCCGCAATTATACATTAA 3101  
 Db 1688 TGCATGACGTTATTATGAGATGGGTTTATGATAGTAGTCCCGCAATTATACATTAA 1747  
 QY 3102 TACGGCATAGAACAAATATGGCGCGCAAATGGGATAATTATCGCGCGGGTGCA 3161  
 Db 1748 TACGGCATAGAACAAATATGGCGCGCAAATGGGATAATTATCGCGCGGGTGCA 1807  
 QY 3162 TCTATGTTACTAGATCGAATT 3183  
 Db 1808 TCTATGTTACTAGATCGAATT 1829

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1863 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO

US-08-525-507-16  
 Query Match 8.1%; Score 257.2; DB 1; Length 1863;  
 Best Local Similarity 98.9%; Pred. No. 5.6e-47;  
 Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2922 CTCGATCGTTAACACATTGGCAATAAGTTCTTAAGATGAACTCTGTGCCGGTCTT 2981  
 Db 1602 CCCGATCGTTCAACATTCGCAATTGGCAATAAGTTCTTAAGATGAACTCCGRTGCCGTCTT 1661  
 QY 2982 GCGATGATTATCATAATTCTGTGAATTACGTAA 3041  
 Db 1662 GCGATGATTATCATAATTCTGTGAATTACGTAA 1721  
 QY 3042 TGCATGACGTTATTATGAGATGGGTTATGAGATTAGCTCTGTGAATTACGTAA 3101  
 Db 1722 TGCATGACGTTATTATGAGATGGGTTATGAGATTAGCTCTGTGAATTACGTAA 1781  
 QY 3102 TAGCGGATAGAAACAAATATGGCGGCAACTGGGATAATTATCGCGCGGGTGTCA 3161  
 Db 1782 TAGCGGATAGAAACAAATATAGCGCGCAACTAGGATAATTATCGCGCGGGTGTCA 1841  
 QY 3162 TCTATGTTACTAGATCGAATC 3183  
 Db 1842 TCTATGTTACTAGATCGAATC 1863

RESULT 11  
 US-08-475-427-9  
 ; Sequence 9, Application US/08475427  
 ; Patent No. 5859340

GENERAL INFORMATION:  
 APPLICANT: DUBOIS, Michel  
 APPLICANT: GRISON, Rene  
 APPLICANT: LEGUAY, Jean-Jacques  
 APPLICANT: PIGNARD, Annie  
 APPLICANT: TOPPAN, Alain  
 TITLE OF INVENTION: Recombinant gene coding for a protein  
 TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington, D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/475,427  
 FILING DATE: 07-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/842,165  
 FILING DATE: 01-MAY-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/FR91/00607  
 FILING DATE: 21-JUL-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 90 09460  
 FILING DATE: 24-JUL-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BENT, Stephen A.  
 REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16781/564/BEDL  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5300  
 TELEFAX: (202) 672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1863 base pairs  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO

US-08-475-427-9  
 Query Match 8.1%; Score 257.2; DB 2; Length 1863;  
 Best Local Similarity 98.9%; pred. No. 5.6e-47;  
 Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2922 CTCGATCGTTAACACATTGGCAATAAGTTCTTAAGATGAACTCTGTGCCGGTCTT 2981  
 Db 1602 CCCGATCGTTCAACATTCGCAATTGGCAATAAGTTCTTAAGATGAACTCCGRTGCCGTCTT 1661  
 QY 2982 GCGATGATTATCATAATTCTGTGAATTACGTAA 3041  
 Db 1662 GCGATGATTATCATAATTCTGTGAATTACGTAA 1721  
 QY 3042 TGCATGACGTTATTATGAGATGGGTTATGAGATTAGCTCTGTGAATTACGTAA 3101  
 Db 1722 TGCATGACGTTATTATGAGATGGGTTATGAGATTAGCTCTGTGAATTACGTAA 1781  
 QY 3102 TAGCGGATAGAAACAAATATGGCGGCAACTGGGATAATTATCGCGCGGGTGTCA 3161  
 Db 1782 TAGCGGATAGAAACAAATATAGCGCGCAACTAGGATAATTATCGCGCGGGTGTCA 1841  
 QY 3162 TCTATGTTACTAGATCGAATC 3183  
 Db 1842 TCTATGTTACTAGATCGAATC 1863

RESULT 12  
 US-07-842-165-9  
 ; Sequence 9, Application US/07842165  
 ; Patent No. 5932698

GENERAL INFORMATION:  
 APPLICANT: DUBOIS, Michel  
 APPLICANT: GRISON, Rene  
 APPLICANT: LEGUAY, Jean-Jacques  
 APPLICANT: PIGNARD, Annie  
 APPLICANT: TOPPAN, Alain  
 TITLE OF INVENTION: Recombinant gene coding for a protein  
 TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FOLEY & LARDNER  
 STREET: King Street Station, Suite 500, 1800 Diagonal  
 STREET: Road, PO Box 299  
 CITY: ALEXANDRIA  
 STATE: VIRGINIA  
 COUNTRY: USA  
 ZIP: 22313-0299  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/842,165  
 FILING DATE: 19920501  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SAXE, Bernhard D  
 REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 16781/348  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 836-9300  
 TELEFAX: (703) 683-4109

INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1863 base Pairs  
 TYPE: NUCLEAR ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 US-07-842-165-9

Query Match 8.1%; Score 257.2; DB 2; Length 1863;  
 Best Local Similarity 98.9%; Pred. No. 5.6e-47; Mismatches 3; Indels 0; Gaps 0;  
 Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2922 CTCGATCGTTCAACATTTGCAATAAGTTCTTAAGATGAAATCCTGTGCCGGTCTT 2981  
 Db 1602 CCCGATCGTTCAACATTTGCAATAAGTTCTTAAGATGAAATCCTGTGCCGGTCTT 1661  
 QY 2982 GCGATGATTATCATATAATTCTCTGTGAAATTACGTTAAGCATGTAATAAACATGAA 3041  
 Db 1662 GCGATGATTATCATATAATTCTCTGTGAAATTACGTTAAGCATGTAATAAACATGAA 1721  
 QY 3042 TGCATGACGTTATTATGAGATGGGTTTATGAGTAGAGTCCCAGAATATACATTAA 3101  
 Db 1722 TGCATGACGTTATTATGAGATGGGTTTATGAGTAGAGTCCCAGAATATACATTAA 1781  
 QY 3102 TACGGATAGAAACAAATATGGCGCGCAACTGGGATAATTATCGCCGCGGTGCA 3161  
 Db 1782 TACGGATAGAAACAAATATAGCGCGCAACTGGGATAATTATCGCCGCGGTGCA 1841  
 QY 3162 TCTATGTTACTAGATCGAATTTC 3183  
 Db 1842 TCTATGTTACTAGATCGAATTTC 1863

RESULT 13

US-08-525-507-14

Sequence 14 Application US/08525507  
 Patent No. 5792932  
 GENERAL INFORMATION:  
 APPLICANT: MARCO, Yves  
 APPLICANT: ROBY, Dominique  
 APPLICANT: SCHNEIDER, Michel  
 APPLICANT: TOPPAN, Alain  
 TITLE OF INVENTION: Plant promoter, microorganisms and plant cells containing a unit for the expression of a protein of title of invention comprising said promoter.  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DENNISON, MESEROLE, POLLACK & SCHEINER  
 STREET: 612 Crystal Square 4 - 1745 Jefferson Davis  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: USA  
 ZIP: 666

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/525,507  
 FILING DATE: 27-JUN-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 93 03299  
 FILING DATE: 23-MAR-1993

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO FR94/00316  
 FILING DATE: 23-MAR-1994  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 412-1155  
 TELEFAX: (703) 412-1161

INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4284 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 US-08-525-507-14

Query Match 8.1%; Score 257.2; DB 1; Length 4284;  
 Best Local Similarity 98.9%; Pred. No. 7.1e-47; Mismatches 3; Indels 0; Gaps 0;  
 Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2922 CTCGATCGTTCAACATTTGCAATAAGTTCTTAAGATGAAATCCTGTGCCGGTCTT 2981  
 Db 4023 CCCGATCGTTCAACATTTGCAATAAGTTCTTAAGATGAAATCCTGTGCCGGTCTT 4082  
 QY 2982 GCGATGATTATCATATAATTCTCTGTGAAATTACGTTAAGCATGTAATAAACATGAA 3041  
 Db 4083 GCGATGATTATCATATAATTCTCTGTGAAATTACGTTAAGCATGTAATAAACATGAA 4142  
 QY 3042 TGCATGACGTTATTATGAGATGGGTTTATGAGTAGAGTCCCAGAATATACATTAA 3101  
 Db 4143 TGCATGACGTTATTATGAGATGGGTTTATGAGTAGAGTCCCAGAATATACATTAA 4202  
 QY 3102 TACGGATAGAAACAAATATGGCGCGCAACTGGGATAATTATCGCCGCGGTGCA 3161  
 Db 4203 TACGGATAGAAACAAATATAGCGCGCAACTGGGATAATTATCGCCGCGGTGCA 4262  
 QY 3162 TCTATGTTACTAGATCGAATTTC 3183  
 Db 4263 TCTATGTTACTAGATCGAATTTC 4284

RESULT 14

US-08-673-768-1

Sequence 1 Application US/08673768  
 Patent No. 5952546  
 GENERAL INFORMATION:  
 APPLICANT: Bedbrook, John R.  
 APPLICANT: Dunsuir, Pamela  
 APPLICANT: Howie, William J.  
 APPLICANT: Joe, Lawrence K.  
 APPLICANT: Lee, Kathleen Y.  
 TITLE OF INVENTION: Delayed Ripening Tomato Plants  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/673,768  
 FILING DATE: 27-JUN-1996  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/000,721  
 FILING DATE: 30-JUN-1995

ATTORNEY/AGENT INFORMATION:  
 NAME: Bastian, Kevin L.  
 REGISTRATION NUMBER: 34,774  
 REFERENCE/DOCKET NUMBER: 012176-005010US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15397 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA

US-08-673-768-1

Query Match 8.0%; Score 256.2; DB 2; Length 15397;  
 Best Local Similarity 92.2%; Pred. No. 1.7e-46;  
 Matches 270; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Matches 270; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2887 CCGTTCGGAATGTATTAGTTACGCCAGCCCTGAGCTCGATCGTCAAACATTGGCAAT 2946  
 10019 CAGGTGGTTCTGAGTTGTTCTAGAGTCAGGGCAGATCGTCAAACATTGGCAAT 10078

QY 2947 AAAGTTCTTAAGATTGATCCTGTGCCGGCTTGCGATGATTATCATATAATTCTGT 3006  
 10079 AAAGTTCTTAAGATTGATCCTGTGCCGGCTTGCGATGATTATCATATAATTCTGT 10138

QY 3007 TGAATTACGTTAACATGTAATAATTACATGTAAATGCAATGGATGGG 3066  
 10139 TGAATTACGTTAACATGTAATAATTACATGTAAATGCAATGGATGGG 10198

Db 3067 TTTTATGATTAGTCCCCTAATTATACATTAAATACGGATAGAAACAAATTATGGC 3126  
 QY 3127 GCGCAAACGTGGATAAATTATCGCGCGGGTGTCACTATGTACTAGATCGA 3179

Db 10199 TTTTATGATTAGTCCCCTAATTATACATTAAATACGGATAGAAACAAATTATAGC 10258  
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Db 10259 GCGCAAACTAGGATAAATTATCGCGCGGGTGTCACTATGTACTAGATCGA 10311

---

RESULT 15  
 US-08-673-768-1/c

Sequence 1, Application US/08673768  
 Patent No. 5952546

GENERAL INFORMATION:

APPLICANT: Bedbrook, John R.  
 APPLICANT: Dunsmuir, Pamela  
 APPLICANT: Howie, William J.  
 APPLICANT: Joe, Lawrence K.  
 APPLICANT: Lee, Kathleen Y.

TITLE OF INVENTION: Delayed Ripening Tomato Plants

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/673, 768  
 FILING DATE: 27-JUN-1996  
 CLASSIFICATION: 800

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/000, 721  
 FILING DATE: 30-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.  
 REGISTRATION NUMBER: 34,774  
 REFERENCE/DOCKET NUMBER: 012176-005010US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15397 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA

US-08-673-768-1

Query Match 8.0%; Score 256.2; DB 2; Length 15397;  
 Best Local Similarity 92.2%; Pred. No. 1.7e-46;  
 Matches 270; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Matches 270; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2887 CCGTTCGGAATGTATTAGTTACGCCAGCCCTGAGCTCGATCGTCAAACATTGGCAAT 2946  
 326 CAGGTGGTTCTGAGTTGTTCTAGAGTCAGGGCAGATCGTCAAACATTGGCAAT 267

QY 2947 AAAGTTCTTAAGATTGATCCTGTGCCGGCTTGCGATGATTATCATATAATTCTGT 3006  
 266 AAAGTTCTTAAGATTGATCCTGTGCCGGCTTGCGATGATTATCATATAATTCTGT 207

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QY 3067 TTTTATGATTAGTCCCCTAATTATACATTAAATACGGATAGAAACAAATTATGGC 3126  
 146 TTTTATGATTAGTCCCCTAATTATACATTAAATACGGATAGAAACAAATTATAGC 87

Db 3127 GCGCAAACGTGGATAAATTATCGCGCGGGTGTCACTATGTACTAGATCGA 3179  
 86 GCGCAAACTAGGATAAATTATCGCGCGGGTGTCACTATGTACTAGATCGA 34

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: June 10, 2004, 05:04:35 ; Search time 5033 Seconds  
(without alignments)  
2886.713 Million cell updates/sec

Title: US-10-072-077A-1

Perfect score: 3183

Sequence: 1 gatatctcttttattatcca.....tatgttactagatcgaaatc 3183

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2998549 seqs, 2282253817 residues

Total number of hits satisfying chosen parameters: 5997098

Post-processing: Minimum Match 0%

Maximum DB seq length: 0

Listing first 45 summaries

Database : Published Applications NA:\*

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- 3: /cgn2\_6/ptodata/2/pubpna/us06 NEW PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/us06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/us08 NEW PUB.seq:\*
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- 10: /cgn2\_6/ptodata/2/pubpna/us09C\_PUBCOMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	3183	100.0	3183	15 US-10-072-077A-1	Sequence 1, Appli
2	733.4	23.0	1988	17 US-10-363-723-2	Sequence 2, Appli
3	730.2	22.9	2595	16 US-10-369-324-3	Sequence 3, Appli
4	730.2	22.9	2595	16 US-10-392-301-3	Sequence 3, Appli
5	730.2	22.9	2595	17 US-10-607-538-3	Sequence 3, Appli
6	730.2	22.9	9323	16 US-10-369-324-4	Sequence 4, Appli
7	730.2	22.9	9323	17 US-10-607-538-4	Sequence 4, Appli
8	714.8	22.5	723	15 US-10-187-339-12	Sequence 12, Appli
9	712.2	22.4	747	15 US-10-187-339-5	Sequence 5, Appli
10	711.8	22.4	720	16 US-10-369-493-38936	Sequence 38936, A
11	711.8	22.4	720	16 US-10-369-493-38940	Sequence 38940, A
12	711.8	22.4	720	16 US-10-369-493-38944	Sequence 38944, A
13	711.8	22.4	720	16 US-10-369-493-38966	Sequence 38966, A
14	630.2	19.8	1997	16 US-10-465-008-1	Sequence 1, Appli

ALGORITHMS

RESULT 1

US-10-072-077A-1

Sequence 1, Application US/10072077A

Publication No. US20030150009A1

GENERAL INFORMATION:

APPLICANT: Gallie, Daniel R.

APPLICANT: Young, Todd E.

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Generation of Multiple Embryo Maize

FILE REFERENCE: 023070-121500US

CURRENT APPLICATION NUMBER: US/10/072,077A

CURRENT FILING DATE: 2002-02-07

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 3183

TYPE: DNA

ORGANISM: Arabidopsis thaliana

FEATURE: promoter

NAME/KEY: promoter

LOCATION: (1)..(3183)

OTHER INFORMATION: senescence-associated gene 12-1 (SAG12-1) promoter

US-10-072-077A-1

Query Match

Best Local Similarity

Score

Pred. No.

Length

DB

ID

100.0%; 3183; 15; 3183;

0; 0; 0; 0; 0; 0;

Matches 3183; Conservative

Indels

Gaps

0; 0; 0; 0; 0; 0;

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Sequence 2, Appli

Sequence 3, Appli

Sequence 4, Appli

Sequence 5, Appli

Sequence 6, Appli

Sequence 7, Appli

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Sequence 59, Appli

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QY	1261	TTTATTTGTTATCTTAATGACAGGGAAACTTCATAAGATGAGATTGG	1320
Db	1261	TTTATTTGTTATCTTAATGACAGGGAAACTTCATAAGATGAGATTGG	1320
QY	1321	GGAAACATCATGAAACAGGAACCTTACAGAAATCATATGATTACAAAGAT	1380
Db	1321	GGAAACATCATGAAACAGGAACCTTACAGAAATCATATGATTACAAAGAT	1380
QY	1381	ACTTAGCGTAATGAACTCTGTTGAATGACTATGATCAAATTGTTAATT	1440
Db	1381	ACTTAGCGTAATGAACTCTGTTGAATGACTATGATCAAATTGTTAATT	1440
QY	1441	TTGTCGAATCATTTCTTTGATTGATAAGCTTTAACTTGCAACGAATGGTTCT	1500
Db	1441	TTGTCGAATCATTTCTTTGATTGATAAGCTTTAACTTGCAACGAATGGTTCT	1500
QY	1501	TGTGAATAACAGAATCTTGAATTCAACTATTGATTAGTAAAGACAAAGAT	1560
Db	1501	TGTGAATAACAGAATCTTGAATTCAACTATTGATTAGTAAAGACAAAGAT	1560
QY	1561	TCCRTGTTTATGTTGATTAGTGTGATTGATGTCACGGATATGTT	540
Db	1561	TCCRTGTTTATGTTGATTGATGTCACGGATATGTT	540
QY	1621	AATAAACATGTACGTAACGATGAAATTGGCATTATTGATTATTTGGCTTAAGGTTGC	600
Db	1621	AATAAACATGTACGTAACGATGAAATTGGCATTATTGATTATTTGGCTTAAGGTTGC	600
QY	1681	TACTCATGATAGATTTTTTGAAATGTCAATTAAAGTATTTCACAAATTAA	1740
Db	1681	TACTCATGATAGATTTTTTGAAATGTCAATTAAAGTATTTCACAAATTAA	1740
QY	1741	TTTAATTAAATAAGGAATATTGCAAAACATCATCACACATATCCAAC	1800
Db	1741	TTTAATTAAATAAGGAATATTGCAAAACATCATCACACATATCCAAC	1800
QY	1801	TGAAATCTTATGACAACTGGTACCTTGTTAAGAAAAGTTGATATAGTTAAC	1860
Db	1801	TGAAATCTTATGACAACTGGTACCTTGTTAAGAAAAGTTGATATAGTTAAC	1860
QY	1861	ATCATCAATTAAATGTTTACAAAGTAGAGAAATTAAACCCACCAACTAAAC	1920
Db	1861	ATCATCAATTAAATGTTTACAAAGTAGAGAAATTAAACCCACCAACTAAAC	1920
QY	1921	CCGAGCAAAGTGAGTAAAGACTTGTGATTTCAGGTGATGTTAGGACTAAATGGCTACG	1980
Db	1921	CCGAGCAAAGTGAGTAAAGACTTGTGATTTCAGGTGATGTTAGGACTAAATGGCTACG	1980
QY	1981	TATCAAACATCAACGATCATTAGTTGATGAACTTGTGACTAGGGGATTCCACATCAA	840
Db	1981	TATCAAACATCAACGATCATTAGTTGATGAACTTGTGACTAGGGGATTCCACATCAA	840
QY	2041	AAAATGCTTGTGATTGGATCACTCACTTGTTAGTGTGAACTTGTGAAACTTGTGAAAC	2040
Db	2041	AAAATGCTTGTGATTGGATCACTCACTTGTTAGTGTGAACTTGTGAAAC	2040
QY	2101	TTTCACTATAACCCATCTCAGCTTCAATTAAACCCATCTCAGCTTCAATTAAACCTTA	2100
Db	2101	TTTCACTATAACCCATCTCAGCTTCAATTAAACCCATCTCAGCTTCAATTAAACCTTA	2100
QY	2161	CATTAACATTCTAACCGGATAGCTTCCAGCAGGGCTTCCAGTCCTTCGCTTGAT	2280
Db	2161	CATTAACATTCTAACCGGATAGCTTCCAGCAGGGCTTCCAGTCCTTCGCTTGAT	2280
QY	2221	AGACGACGACGGGATAGCTTCCAGCAGGGCTTCCAGTCCTTCGCTTGAT	2340
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QY	2281	CGGGTCAAATCGTGTCTCAACTAACCGGAGGGACCAACAGTGGAAACTG	2280
Db	2281	CGGGTCAAATCGTGTCTCAACTAACCGGAGGGACCAACAGTGGAAACTG	2280

QY 2341 AAAGGAACGACGGCTCTACCTTGATGATCGGCCTCTGGTGGAGGTATCATCGCAGCC 2400 ; APPLICANT: HEAZLEWOOD, Joshua W.  
Db 2341 AAAGGAACGACGGCTCTACCTTGATGATCGGCCTCTGGTGGAGGTATCATCGCAGCC 2400 ; TITLE OF INVENTION: Manipulation of plant senescence  
; FILE REFERENCE: 14403US  
; CURRENT APPLICATION NUMBER: US/10/363,723  
; CURRENT FILING DATE: 2003-03-05  
; PRIORITY APPLICATION NUMBER: AU PQ9946  
; PRIORITY FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 1988  
; TYPE: DNA  
; ORGANISM: Agrobacterium tumefaciens  
; US-10-363-723-2

QY 2521 GCGAGATTTCGTTGGCATATTTCGCCACAAGTACCCGACCAAGAACGCTTCATGAAA 2580  
Db 2521 GCAGATTTCGTTGGCATATTTCGCCACAAGTACCCGACCAAGAACGCTTCATGAAA 2580

QY 2581 GCGGCCAAGGCCAGAGTTAACGAGATCGCACCCGCTGAGGCCATTCTCAA 2640  
Db 2581 GCGGCCAAGGCCAGAGTTAACGAGATCGCACCCGCTGAGGCCATTCTCAA 2640

QY 2641 GAGTRGGTTATCTTGGAATGAACTCGGCTGAGGCCATTCTGA 2700  
Db 2641 GAGTRGGTTATCTTGGAATGAACTCGGCTGAGGCCATTCTGA 2700

QY 2701 TATCGATATGCCATGTTGCTGAGATCGGACCTCGGCTGAGGCCATTCTGA 2760  
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QY 2761 CTRGACGCAATATGGAAAGTAATGGATCGGATCGCTCAGGATTTCCAT 2820  
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QY 2821 GGGGCCAACAGAACAGAAATCCCCAACGGCTTACGCCAGCGCTTCCACCGA 2880  
Db 2821 GGGGCCAACAGAACAGAAATCCCCAACGGTAAACGCCAGCGCTTCCACCGA 2880

QY 2881 GGTCAATCCGGTCCGAATGTTACGCCAGCCCTGAGCTCGATCGTTCAAACATT 2940  
Db 2881 GGTCAATCCGGTCCGAATGTTACGCCAGCCCTGAGCTCGATCGTTCAAACATT 2940

QY 2941 GGCATAAAAGTTCTTAAGATGAACTCTGTGCGATGATATCATATAAT 3000  
Db 2941 GGCATAAAAGTTCTTAAGATGAACTCTGTGCGATGATATCATATAAT 3000

QY 3001 TTCTGTGAAATTACGTTAACATGATGACGTTATTATGA 3060  
Db 3001 TTCTGTGAAATTACGTTAACATGATGACGTTATTATGA 3060

QY 3061 GATGGTTTATGATTAGACTCCGCAATTACATTAAACGGATAGAAACAAA 3120  
Db 3061 GATGGTTTATGATTAGACTCCGCAATTACATTAAACGGATAGAAACAAA 3120

QY 3121 TATGGCGCGCAACTGGATAATTACGGCGGTGTCATCTATGTTACTAGATCGAA 3180  
Db 3121 TATGGCGCGCAACTGGATAATTACGGCGGTGTCATCTATGTTACTAGATCGAA 3180

QY 3181 TTC 3183  
Db 3181 TTC 3183

RESULT 2  
US-10-363-723-2  
; Sequence 2, Application US/10363723  
; Publication No. US20040025205A1  
; GENERAL INFORMATION:  
; APPLICANT: Agriculture Victoria Services Pty Ltd  
; APPLICANT: La Trobe University  
; APPLICANT: SPANGENBERG, German  
; APPLICANT: LIN, Yi Han  
; APPLICANT: PARISH, Roger W.  
; APPLICANT: LI, Song Feng W.

QY 2739 CACGGCAGATATGCTATGCCATGGAGGATATGCCATGGTGGAGGAT 2798  
Db 1247 CACGGCAGATATGCTATGCCATGGAGGATATGCCATGGTGGAGGAT 1306

QY 2799 CGCTCAGGAGTATTCCATGGAGGATATGCCATGGAGGATATGCCATGGTGGAGGAT 2858  
Db 1307 CGCTCAGGAGTATTCCATGGAGGATATGCCATGGAGGATATGCCATGGTGGAGGAT 1366

QY 2859 AGCCGCTTCGAGGATTCACTGGATGTTACGGCCAGCCCT 2918  
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QY . 2919 GAG 2921  
Db 1427 GCG 1429

RESULT 3  
US-10-369-324-3  
; Sequence 3, Application US/10369324  
; Publication No. US20030221213A1  
; GENERAL INFORMATION:  
; APPLICANT: ROMMENS, CAIUS  
; APPLICANT: YE, JINGSONG  
; APPLICANT: MENENDEZ-HUMARA, JAIME  
; APPLICANT: YAN, HUA  
; APPLICANT: RICHARD, CRAIG  
; APPLICANT: BRINKERHOFF, W. LEIGH  
; APPLICANT: SWORDS, KATHY M. M.  
; TITLE OF INVENTION: PRECISE BREEDING  
; FILE REFERENCE: 058951/0162  
; CURRENT APPLICATION NUMBER: US/10/369, 324  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/357, 661  
; PRIORITY FILING DATE: 2002-02-20  
; PRIORITY FILING DATE: 2002-05-06  
; NUMBER OF SEQ ID NOS: 124  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2595  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Expression  
; OTHER INFORMATION: cassette for the IPT gene  
; US-10-369-324-3

Query Match 22.9%; Score 730.2; DB 16; Length 2595;  
Best Local Similarity 99.6%; Pred. No. 1.4e-124;  
Matches 732; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2187 CCTGCATCTAATTTCGGTCCAACTTGCACAGGAAGACGACGACCGCGATAGCTCTGC 2246  
Db 1166 CCTGCATCTAATTTCGGTCCAACTTGCACAGGAAGACGACGACCGCGATAGCTCTGC 1225

QY 2247 CCAGCAGACAGGGCTCCAGTCTTCGGTCAATCGTGTCTCAACTAC 2306  
Db 1226 CCAGCAGACAGGGCTCCAGTCTTCGGTCAATCGTGTCTCAACTAC 1285

QY 2307 AACCGGAAGGGGACCAACAGTGGAAAGAACGGAAACGGACGGGTCTACCTG 2366  
Db 1286 AACCGGAAGGGGACCAACAGTGGAAAGAACGGAAACGGACGGGTCTACCTG 1345

QY 2367 TGATCGGCCTCTGGTGGAGGGTATCATCGCAGCAAGCAAGCTCATCATGGCTGATCGA 2426  
Db 1346 TGATCGGCCTCTGGTGGAGGGTATCATCGCAGCAAGCAAGCTCATCATGGCTGATCGA 1405

QY 2427 GGAGGTGTATAATCATGAGGCCAACGGGGCTTATTCTGGGGAGGATCCACCTCGTT 2486  
Db 1406 GGAGGTGTATAATCATGAGGCCAACGGGGCTTATTCTGGGGAGGATCCACCTCGTT 1465

QY 2487 GCTCAACTGCATGGGGGAAACAGCTTATGGAGTGCAGATTCTGGTGGCATATATCG 2546  
Db 1466 GCTCAACTGCATGGGGGAAACAGCTTATGGAGTGCAGATTCTGGTGGCATATATCG 1525

QY 2547 CCACAAGTTACCCGACCAAGAGACCTTCATGAAAGGGCAAGGCCAAGCGAT 2606  
Db 1526 CCACAAGTTACCCGACCAAGAGACCTTCATGAAAGGGCAAGGCCAAGCGAT 1585

QY 2607 GTTGACCCCCGGTGCAGGCCATTCTTCAAGAGTTGGTTATCTTGGATGAC 2666  
Db 1586 GTTGACCCCCGGTGCAGGCCATTCTTCAAGAGTTGGTTATCTTGGATGAC 1645

QY 2667 TCGGCTGAGGCCATTCTGAAAGAGATCGATGGATATGCCATGTGTTGCTAG 2726

Db 1646 TCGGCTGAGGCCATTCTGAAAGAGATCGATGGATATGCCATGTGTTGCTAG 1705  
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Db 1706 CCAGAACCGAGATCACGGCAGATATGCTATTCGAGCTTGACGCCAATATGGAAGGTAAGTT 1765

RESULT 4  
US-10-392-301-3  
; Sequence 3, Application US/10392301  
; Publication No. US20040003434A1  
; GENERAL INFORMATION:  
; APPLICANT: WEEKS, J. TROY  
; TITLE OF INVENTION: REFINED PLANT TRANSFORMATION  
; FILE REFERENCE: 058951/0164  
; CURRENT APPLICATION NUMBER: US/10/392, 301  
; CURRENT FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: 60/365, 527  
; PRIORITY FILING DATE: 2002-03-20  
; PRIORITY FILING DATE: 2002-05-06  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2595  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Cytokinin IPT  
; OTHER INFORMATION: gene plasmid  
; US-10-392-301-3

Query Match 22.9%; Score 730.2; DB 16; Length 2595;  
Best Local Similarity 99.6%; Pred. No. 1.4e-124;  
Matches 732; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2187 CCTGCATCTAATTTCGGTCCAACCTGGACAGGAAGACGGACGGGTCTACCTG 2246  
Db 1166 CCTGCATCTAATTTCGGTCCAACCTGGACAGGAAGACGGACGGGTCTACCTG 1225

QY 2247 CCAGCAGACAGGGCTCCAGTCTTCGGTCAATCGTGTCTCAACTAC 2306  
Db 1226 CCAGCAGACAGGGCTCCAGTCTTCGGTCAATCGTGTCTCAACTAC 1285

QY 2307 AACCGGAAGGGGACCAACAGTGGAAAGAACGGAAACGGACGGGTCTACCTG 2366  
Db 1286 AACCGGAAGGGGACCAACAGTGGAAAGAACGGAAACGGACGGGTCTACCTG 1345

QY 2367 TGATCGGCCTCTGGTGGAGGGTATCATCGCAGCAAGCAAGCTCATCATGGCTGATCGA 2426  
Db 1346 TGATCGGCCTCTGGTGGAGGGTATCATCGCAGCAAGCAAGCTCATCATGGCTGATCGA 1405

QY 2427 GGAGGTGTATAATCATGAGGCCAACGGGGCTTATTCTGGGGAGGATCCACCTCGTT 2486  
Db 1406 GGAGGTGTATAATCATGAGGCCAACGGGGCTTATTCTGGGGAGGATCCACCTCGTT 1465

QY 2487 GCTCAACTGCATGGGGGAAACAGCTTATGGAGTGCAGATTCTGGTGGCATATATCG 2546  
Db 1466 GCTCAACTGCATGGGGGAAACAGCTTATGGAGTGCAGATTCTGGTGGCATATATCG 1525

QY 2547 CCACAAGTTACCCGACCAAGAGACCTTCATGAAAGGGCAAGGCCAAGCGAT 2606  
Db 1526 CCACAAGTTACCCGACCAAGAGACCTTCATGAAAGGGCAAGGCCAAGCGAT 1585

QY 2607 GTTGACCCCCGGTGCAGGCCATTCTTCAAGAGTTGGTTATCTTGGATGAC 2666  
Db 1586 GTTGACCCCCGGTGCAGGCCATTCTTCAAGAGTTGGTTATCTTGGATGAC 1645

QY 2667 TCGGCTGAGGCCATTCTGAAAGAGATCGATGGATATGCCATGTGTTGCTAG 2726

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Db 1526 CCACAAAGTTACCCGACCAAGAGACCTTCATGAAGGGCCAAGGCCAGAGTTAACGAGAT 1585

QY 2607 GTRGCACCCCGCTGCAGGCATTCTTCAAGAGTTACCTTGTGAATGAAACC 2666  
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QY 2667 TCGGTGAGGCCATTCTGAAAGAGATCGATGGATATGCCATGGTTGTCTAG 2726  
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QY 2727 CCAGAACAGATCACGGCAGATAGCTATGCACTTGAGGATATGCCATGGTTGTCTAG 2786  
Db 1705 CCAGAACAGATCACGGCAGATAGCTATGCACTTGAGGATATGCCATGGTTGTCTAG 1765

QY 2787 GATTATGGATCGCTCAGGAGTATTCTCATCCATGCGGGCAACAGGAATTC 2846  
Db 1766 GATTATGGATCGCTCAGGAGTATTCTCATCCATGCGGGCAACAGGAATTC 1825

QY 2847 CCAAGTTAACGCCAGAGACCTTCGACGGATTCGAAGGTATCCGTTCGGAATGTTAGGT 2906  
Db 1826 CCAAGTTAACGCCAGAGACCTTCGACGGATTCGAAGGTATCCGTTCGGAATGTTAGGT 1885

QY 2907 TACGCCAGCCCTGAG 2921  
Db 1886 TACGCCAGCCCTGAG 1900

RESULT 5  
US-10-607-538-3  
; Sequence 3, Application US/10607538  
; Publication No. US20040107455A1  
; GENERAL INFORMATION:  
; APPLICANT: ROMMENS, CAIUS  
; APPLICANT: YE, JINGSONG  
; APPLICANT: HUMARA, JAIME M.  
; APPLICANT: YAN, HUA  
; APPLICANT: SWORDS, KATHY  
; TITLE OF INVENTION: PRECISE BREEDING  
; FILE REFERENCE: 058951/0167  
; CURRENT APPLICATION NUMBER: US/10/607,538  
; CURRENT FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: 10/369,324  
; PRIOR FILING DATE: 2003-02-20  
; PRIORITY NUMBER: 60/357,661  
; PRIORITY FILING DATE: 2002-02-20  
; PRIORITY APPLICATION NUMBER: 60/377,602  
; PRIORITY FILING DATE: 2002-05-06  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 3  
; LENGTH: 2595  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Expression  
; US-10-607-538-3

Query Match 22.9%; Score 730.2; DB 17; Length 2595;  
Best Local Similarity 99.6%; Pred. No. 1.4e-124;  
Matches 732; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2187 CCTGCATCTAATTTCGGTCAACTTGCACAGGAAGACCGACGGCATAGCTCTGC 2246  
Db 1166 CCTGCATCTAATTTCGGTCAACTTGCACAGGAAGACCGACGGCATAGCTCTGC 1225

QY 2247 CGAGCAGACAGGGCTTCAGTCTGCTGCTCAACTTC 2306  
Db 1226 CCAGCAGACAGGGCTTCAGTCTGCTGCTCAACTTC 1285

QY 2307 AACCGGAGCCACGACCAACTTGAAGGAACGACCGCGCTCTACCTTGA 2366  
Db 1286 AACCGGAAGCCGACGACCAACTTGAAGGAACGACCGCGCTCTACCTTGA 1345

QY 2367 TGATCGCCTCTGGGAGGGTATCATCCAGCCAGCAAGCTCATAGGTGATCGA 2426  
Db 1346 TGATCGCCTCTGGGAGGGTATCATCCAGCCAGCAAGCTCATAGGTGATCGA 1405

QY 2427 GGAGGTGATAATCATGAGGCCAACGGCGCTTATCTTGAGGAGATCACCTCGTT 2486  
Db 1406 GGAGGTGATAATCATGAGGCCAACGGCGCTTATCTTGAGGAGATCACCTCGTT 1465

QY 2487 GCTCAACTGCATGGCGCAAACAGCTATTGGAGTGCAGTTGAGGATTCACCTCGTT 2546  
Db 1466 GCTCAACTGCATGGCGCAAACAGCTATTGGAGTGCAGTTGAGGATTCACCTCGTT 1525

QY 2547 CCACAAGTTACCCGCCAGAGACCTTCGACGGATTCGAAGGTATCCGTT 2606  
Db 1526 CCACAAGTTACCCGCCAGAGACCTTCGACGGATTCGAAGGTATCCGTT 1645

QY 2667 TCGGTGAGGCCATTCTGAAAGAGATCGATGGATATGCCATGGTTGTCTAG 2726  
Db 1705 TCGGTGAGGCCATTCTGAAAGAGATCGATGGATATGCCATGGTTGTCTAG 1765

QY 2727 CCAGAACAGATCACGGCAGATAGCTATGCACTTGAGGATATGCCATGGTTGTCTAG 2786  
Db 1786 CCAGAACAGATCACGGCAGATAGCTATGCACTTGAGGATATGCCATGGTTGTCTAG 1885

QY 2847 CCAAGTTAACGCCAGAGACCTTCGACGGATTCGAAGGTATCCGTT 2906  
Db 1826 CCAAGTTAACGCCAGAGACCTTCGACGGATTCGAAGGTATCCGTT 1885

QY 2907 TACGCCAGCCCTGAG 2921  
Db 1886 TACGCCAGCCCTGAG 1900

RESULT 6  
US-10-369-324-4  
; Sequence 4, Application US/10369324  
; Publication No. US20030221213A1  
; GENERAL INFORMATION:  
; APPLICANT: ROMMENS, CAIUS  
; APPLICANT: YE, JINGSONG  
; APPLICANT: MENENDEZ-HUMARA, JAIME  
; APPLICANT: RICHARD, CRAIG  
; APPLICANT: BRINKERHOFF, W. LEIGH  
; APPLICANT: SWORDS, KATHY M. M.  
; TITLE OF INVENTION: PRECISE BREEDING  
; FILE REFERENCE: 058951/0162  
; CURRENT APPLICATION NUMBER: US/10/369,324  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/357,661  
; PRIORITY FILING DATE: 2002-02-20  
; PRIORITY APPLICATION NUMBER: 60/377,602  
; PRIORITY FILING DATE: 2002-05-06  
; NUMBER OF SEQ ID NOS: 124  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 9323  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: psim11

; OTHER INFORMATION: nucleotide sequence  
US-10-369-324-4

Query Match 22.9%; Score 730.2; DB 16; Length 9323;  
Best Local Similarity 99.6%; Pred. No. 2.5e-124;  
Matches 732; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY |||||  
Db 7646 CCTGCATCTAATTTCGGTCCAACTTGCAAGGAAAGACGACGACGCCGATACTCTGC 2246  
QY |||||  
Db 7646 CCTGCATCTAATTTCGGTCCAACTTGCAAGGAAAGACGACGACGCCGATACTCTGC 7705

QY 2247 CCTGCATCTAATTTCGGTCCAACTTGCAAGGAAAGACGACGACGCCGATACTCTGC 2246  
Db 7706 CCAGCAGACAGGGCTCCAGTCCTTCGCTTGATCGGGTCAAATGCTCTACTATC 7765

QY 2307 AACCGGAAGGGGACGACCAACAGTGGAAAGAACGAGCGGTCTACTTGA 2366  
Db 7766 AACCGGAAGGGGACGACCAACAGTGGAAAGAACGAGCGGTCTACTTGA 7825

QY 2367 TGATCGGCCTCTGGTGGAGGGTATCATCGCAGCCAAAGCAAGGCAAGCTCATCATAGGCTGATCGA 2426  
Db 7826 TGATCGGCCTCTGGTGGAGGGTATCATCGCAGCCAAAGCAAGGCAAGCTCATCATAGGCTGATCGA 7885

QY 2427 GGAGGTGTATAATCATGAGGGCAACAGCTATTGGACTGCAGATTTCGTTGCCATATTATCG 2486  
Db 7886 GGAGGTGTATAATCATGAGGGCAACAGCTATTGGACTGCAGATTTCGTTGCCATATTATCG 7945

QY 2487 GCTCAACTGCATGGCGGAAACAGCTATTGGACTGCAGATTTCGTTGCCATATTATCG 2546  
Db 7946 GCTCAACTGCATGGCGGAAACAGCTATTGGACTGCAGATTTCGTTGCCATATTATCG 8005

QY 2547 CCACAAAGTACCCGACCAAGAGACCTCATGAAGGGCCAAGGGCCAGAGTAAGCAGAT 2606  
Db 8006 CCACAAAGTACCCGACCAAGAGACCTCATGAAGGGCCAAGGGCCAGAGTAAGCAGAT 8065

QY 2607 GTTGCACCCCGCTGCAGGCCATTCTTCAAGAGTGTGTTATCTTGAATGAACC 2666  
Db 8066 GTTGCACCCCGCTGCAGGCCATTCTTCAAGAGTGTGTTATCTTGAATGAACC 8125

QY 2667 TCGGCTGAGGCCATTCTGAAGAGATCGATGGATATCGATGCTATGTTGCTAG 2726  
Db 8126 TCGGCTGAGGCCATTCTGAAGAGATCGATGGATATCGATGCTATGTTGCTAG 8185

QY 2727 CCAGAACAGATCACGGCAGATATGCTATTGCACTGCAAAATATGGAAAGGTAGTT 2786  
Db 8186 CCAGAACAGATCACGGCAGATATGCTATTGCACTGCAAAATATGGAAAGGTAGTT 8245

QY 2787 GATTAATGGGATCGCTCAGGAGTATTCTCATGGGCAACAGGAACAGAACATCCC 2846  
Db 8246 GATTAATGGGATCGCTCAGGAGTATTCTCATGGGCAACAGGAACAGAACATCCC 8305

QY 2847 CCAAGTTAACCGCAGCCGTTTCGACGGATTGCAAGGTCACTGGTTCGGAATGTATTAGT 2906  
Db 8306 CCAAGTTAACCGCAGCCGTTTCGACGGATTGCAAGGTCACTGGTTCGGAATGTATTAGT 8365

QY 2907 TACGCCAGCCCTGAG 2921  
Db 8366 TAGGCCAGCCCTGCG 8380

RESULT 7  
US-10-607-538-4

; Sequence 4, Application US/10607538  
; Publication No. US20040107455A1  
; GENERAL INFORMATION:  
; APPLICANT: ROMMENS, CAIUS  
; APPLICANT: YE, JINGSONG  
; APPLICANT: HUMARA, JAIME M.  
; APPLICANT: YAN, HUA  
; APPLICANT: SWORDS, KATHY  
; TITLE OF INVENTION: PRECISE BREEDING  
; FILE REFERENCE: 058951/0167  
; CURRENT APPLICATION NUMBER: US/10/607,538

CURRENT FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: 10/369,324  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/357,661  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: 60/377,602  
PRIOR FILING DATE: 2002-05-06  
NUMBER OF SEQ ID NOS: 139  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 4

LENGTH: 9323  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: pSIM11  
US-10-607-538-4

Query Match 22.9%; Score 730.2; DB 17; Length 9323;  
Best Local Similarity 99.6%; Pred. No. 2.5e-124;  
Matches 732; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY |||||  
Db 7646 CCTGCATCTAATTTCGGTCCAACCTGCAAGGAAAGACGACGCCGATACTCTGC 2246  
QY |||||  
Db 7706 CCAGCAGACAGGGCTCCAGTCCTTGGCTTGATGGGTCAAATGCTCTCAACTATC 7765

QY 2247 CCAGCAGACAGGGCTCCAGTCCTTGGCTTGATGGGTCAAATGCTCTCAACTATC 2306  
Db 7766 AACCGGAAGGGGACGACCAACAGTGGAAAGAACGAGCGGTCTACTTGA 7825

QY 2307 AACCGGAAGGGGACGACCAACAGTGGAAAGAACGAGCGGTCTACTTGA 2366  
Db 7826 TGATCGGCCTCTGGTGGAGGGTATCATCGCAGCCAAAGCAAGGCAAGCTCATCATAGGCTGATCGA 7885

QY 2367 TGATCGGCCTCTGGTGGAGGGTATCATCGCAGCCAAAGCAAGGCAAGCTCATCATAGGCTGATCGA 7885  
Db 7886 GGAGGTGTATAATCATGAGGGCAACAGCTATTGGACTGCAGATTTCGTTGCCATATTATCG 7945

QY 2427 GGAGGTGTATAATCATGAGGGCAACAGCTATTGGACTGCAGATTTCGTTGCCATATTATCG 2486  
Db 7946 GCTCAACTGCATGGGGCAACAGCTATTGGACTGCAGATTTCGTTGCCATATTATCG 8005

QY 2487 GCTCAACTGCATGGGGCAACAGCTATTGGACTGCAGATTTCGTTGCCATATTATCG 2546  
Db 8006 CCACAAAGTACCCGACCAAGAGACCTCATGAAGGGCCAAGGGCCAGAGTAAGCAGAT 8065

QY 2547 CCACAAAGTACCCGACCAAGAGACCTCATGAAGGGCCAAGGGCCAGAGTAAGCAGAT 2606  
Db 8066 GTTGCACCCCGCTGCAGGCCATTCTTCAAGAGTGTGTTATCTTGGATGAACC 8125

QY 2607 GTTGCACCCCGCTGCAGGCCATTCTTCAAGAGTGTGTTATCTTGGATGAACC 2666  
Db 8126 TCGGCTGAGGCCATTCTGAAGAGATCGATGGATATCGATGCTATGCTGTTGCTAG 8185

QY 2667 TCGGCTGAGGCCATTCTGAAGAGATCGATGGATATCGATGCTATGCTGTTGCTAG 2726  
Db 8246 TCGGCTGAGGCCATTCTGAAGAGATCGATGGATATCGATGCTATGCTGTTGCTAG 8305

QY 2727 CCAGAACAGATCACGGCAGATATGCTATTGCACTGCAAAATATGGAAAGGTAGTT 2786  
Db 8306 CCAGAACAGATCACGGCAGATATGCTATTGCACTGCAAAATATGGAAAGGTAGTT 8365

QY 2787 GATTAATGGGATCGCTCAGGAGTATTCTCATGGGCAACAGGAACAGAACATCCC 2846  
Db 8366 TAGGCCAGCCCTGCG 8380

RESULT 8  
US-10-187-339-12  
; Sequence 12, Application US/10187339  
; Publication No. US20030084478A1

; GENERAL INFORMATION:  
; APPLICANT: Ream, Walt et al.,  
; TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and  
; Methods and Compositions for Producing the Same  
; FILE REFERENCE: 53629  
; CURRENT APPLICATION NUMBER: US/10/187, 339  
; CURRENT FILING DATE: 2002-06-28  
; PRIORITY APPLICATION NUMBER: US/09/434, 837  
; PRIORITY FILING DATE: 1999-11-04  
; PRIORITY APPLICATION NUMBER: 60/107, 185  
; PRIORITY FILING DATE: 1998-11-05  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 723  
; TYPE: DNA  
; ORGANISM: Agrobacterium tumefaciens  
; US-10-187-339-12

Query Match 22.5%; Score 714.8; DB 15; Length 723;  
Best Local Similarity 99.7%; Pred. No. 5.2e-122;  
Matches 716; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2187 CCTGCATCTAATTTCGGTCAACTTGACAGGAAGACGACGGCATAGCTCTTGC 2246  
Db 6 CCTGCATCTAATTTCGGTCAACTTGACAGGAAGACGACGGCATAGCTCTTGC 65

QY 2247 CCAGCAGACAGGGCTTCCAGTGTCTCGCTCACAGGAAGACGACGGCATAGCTCTTGC 2306  
Db 66 CCAGCAGACAGGGCTTCCAGTGTCTCGCTCACAGGAAGACGACGGCATAGCTCTTGC 125

QY 2307 AACCGGAAGCGGAGACCAACAGTGGAAACTGAAAGAACGACGCGTCTCTACCTTGA 2366  
Db 126 AACCGGAAGCGGAGACCAACAGTGGAAACTGAAAGAACGACGCGTCTCTACCTTGA 185

QY 2367 TGATCGGCTCTGGAGGGTATCATCGCAGCAAAGCAAGTCATCATAGGCTGATCGA 2426  
Db 186 TGATCGGCTCTGGAGGGTATCATCGCAGCAAAGTCATCATAGGCTGATCGA 245

QY 2427 GGAGGGTATAATCATGAGGCCAACGGGGCTTATCTGGAGGGATCCACCTCGTT 2486  
Db 246 GGAGGGTATAATCATGAGGCCAACGGGGCTTATCTGGAGGGATCCACCTCGTT 305

QY 2487 GCTCAACTGCATGGCGCGAACAGCTATTGGAGTGCAGATTTCGTGGCATATTTCG 2546  
Db 306 GCTCAACTGCATGGCGCGAACAGCTATTGGAGTGCAGATTTCGTGGCATATTTCG 365

QY 2547 CCACAAAGTACCCGACCAAGAGACCTTATGGAGGCTTATGGAGGATTCAGGAGAT 2606  
Db 366 CCACAAAGTACCCGACCAAGAGACCTTATGGAGGATTCAGGAGAT 425

QY 2607 GRTGACCCCCGCTGCAGGCCATTCTTCAAGAGTTGGTTATCTTGGATGAAAC 2666  
Db 426 GRTGACCCCCGCTGCAGGCCATTCTTCAAGAGTTGGTTATCTTGGATGAAAC 485

QY 2667 TCGGTGAGGCCATTCTGAAAGAGATCGATGGATATGCCATTGTTGGTAG 2726  
Db 486 TCGGTGAGGCCATTCTGAAAGAGATCGATGGATATGCCATTGTTGGTAG 545

QY 2727 CCAGAACCGATCAGGGAGATATGCATTGGCAGGTTGACGAAATATGAAAGTAGTT 2786  
Db 546 CCAGAACCGATCAGGGAGATATGCATTGGCAGGTTGACGAAATATGAAAGTAGTT 605

QY 2787 GATTAAATGGGATCGAGGATATTCCATGCCAACAGGAAAGAAATTCCC 2846  
Db 606 GATTAAATGGGATCGCTCAGGAGTATTCCATGCCAACAGGAAACAGAAATTCCC 665

QY 2847 CCAAGTTAACCGCAGCCGTTTCGACGGATTCGAAGGTCATCCGTCGGAATGTTAG 2904  
Db 666 CCAAGTTAACCGCAGCCGTTTCGACGGATTCGAAGGTCATCCGTCGGAATGTTAG 723

RESULT 9  
US-10-187-339-5  
; Sequence 5, Application US/10187339  
; Publication No. US20030084478A1

; GENERAL INFORMATION:  
; APPLICANT: Ream, Walt et al.,  
; TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and  
; Methods and Compositions for Producing the Same  
; FILE REFERENCE: 53629  
; CURRENT APPLICATION NUMBER: US/10/187, 339  
; CURRENT FILING DATE: 2002-06-28  
; PRIORITY APPLICATION NUMBER: US/09/434, 837  
; PRIORITY FILING DATE: 1999-11-04  
; PRIORITY APPLICATION NUMBER: 60/107, 185  
; PRIORITY FILING DATE: 1998-11-05  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 747  
; TYPE: DNA  
; ORGANISM: Agrobacterium tumefaciens  
; US-10-187-339-5

Query Match 22.4%; Score 712.2; DB 15; Length 747;  
Best Local Similarity 99.6%; Pred. No. 1.6e-121;  
Matches 714; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2188 CTGCATCTAATTTCGGTCCAATCTGCACAGGAAGACGACGGACCGCGATAGCTCTTGC 2247  
Db 18 CTGAATCTAATTTCGGTCCAATCTGCACAGGAAGACGACGGACCGCGATAGCTCTTGC 77

QY 2248 CAGCAGACAGGGCTTCCAGTCTTCGCTGTATCGGTCATCGGTCATCGTCTCAACTATCA 2307  
Db 78 CAGCAGACAGGGCTTCCAGTCTTCGCTGTATCGGTCATCGTCTCAACTATCA 137

QY 2308 ACCGGAAAGCGGACGACCAACAGTGGAAAGAAACTGAAAGAACGACGCGTCTCTACCTTGA 2367  
Db 138 ACCGGAAAGCGGACGACCAACAGTGGAAAGAAACTGAAAGAACGACGCGTCTCTACCTTGA 197

QY 2368 GATCGGCTCTGGAGGGTATCATCGCAGCAAAGCAAGCTCATCATAGGCTGATCGAG 2427  
Db 198 GATCGGCTCTGGAGGGTATCATCGCAGCAAAGCAAGCTCATCATAGGCTGATCGAG 257

QY 2428 GAGGTGTATAATCATGAGGCCAACGGGGCTTATCTTGAGGGAGATCCACCTCGTT 2487  
Db 258 GAGGTGTATAATCATGAGGCCAACGGGGCTTATCTTGAGGGAGATCCACCTCGTT 317

QY 2488 CTCAACTGCATGGCGCGAACAGCTATTGGAGTGCAGATTTCGTGGCATATTATCGC 2547  
Db 318 CTCAACTGCATGGCGCGAACAGCTATTGGAGTGCAGATTTCGTGGCATATTATCGC 377

QY 2548 CACAAGTTACCCGACCAAGAGACCTTATGAAAGGCGCAAGGCCAGAGTTAGCAGAT 2607  
Db 378 CACAAGTTACCCGACCAAGAGACCTTATGAAAGGCGCAAGGCCAGAGTTAGCAGAT 437

QY 2608 TTGCAACCCGCTGCAGGCCATTCTTCAAGAGTTGGTTATCTTGGATGAAAC 2667  
Db 438 TTGCAACCCGCTGCAGGCCATTCTTCAAGAGTTGGTTATCTTGGATGAAAC 497

QY 2668 CGGCTGAGGCCATTCTGAAAGAGATCGATGGATATGCCATTGTTGCTAGC 2727  
Db 498 CGGCTGAGGCCATTCTGAAAGAGATCGATGGATATGCCATTGTTGCTAGC 557

QY 2728 CAGAACCGATCAGGGAGATATGCATTGGCAGCTTGCAGCAATATGAAAGTAGTT 2787  
Db 558 CAGAACCGATCAGGGAGATATGCATTGGCAGCTTGCAGCAATATGAAAGTAGTT 617

QY 2788 ATTAATGGGATCGCTCAGGAGTATTCCATGCCAACAGGAAACAGAAATTCCC 2847

Db 618 ATTATGGATCGCTCAGGAGTATTCCATGGCGCCACAGGAACAGAACATCCCC 677  
 QY 2848 CAAGTTAACGCAGCCGCTTCGACGGATTGAGTCATCCGGTTGGAAATGTATTAG 2904  
 Db 678 CAAGTTAACGCAGCCGCTTCGACGGATTGAGTCATCCGGTTGGAAATGTATTAG 734

RESULT 10  
 US-10-369-493-38936  
 ; Sequence 38936, Application US/10369493  
 ; Publication No. US20030233675A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Goldman, Barry S.  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 ; CURRENT APPLICATION NUMBER: US/10/369, 493  
 ; PRIORITY FILING DATE: 2003-02-28  
 ; PRIORITY FILING DATE: 2002-02-21  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO 38936  
 ; LENGTH: 720  
 ; TYPE: DNA  
 ; ORGANISM: Agrobacterium tumefaciens  
 ; US-10-369-493-38936

Query Match 22.4%; Score 711.8; DB 16; Length 720;  
 Best Local Similarity 99.7%; Pred. No. 1.9e-121;  
 Matches 713; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2187 CCTGCATCTAATTCGGTCCAACCTGCAAGGAAAGACGGACGACGGGATAGCTCTTGC 2246  
 Db 6 CCTGCATCTAATTCGGTCCAACCTGCAAGGAAAGACGGACGACGGGATAGCTCTTGC 65

QY 2247 CCAGCAGACAGGGCTCCAGTCTCTTGCGTCTGATCGGTCCAATCGTGTCTCAACTATC 2306  
 Db 66 CCAGCAGACAGGGCTCCAGTCTCTTGCGTCTGATCGGTCCAATCGTGTCTCAACTATC 125

QY 2307 AACCGGAAGGGGACGACCAACAGTGGAAAGAACTGAAGAACGAGCGGTCTCTACCTTGA 2366  
 Db 126 AACCGGAAGGGGACGACCAACAGTGGAAAGAACGAGCGGTCTCTACCTTGA 185

QY 2367 TGATCGGCCCTCTGGGAGGGTATCATGCCAGCAAGCAAGCTCATAGGTGATCGA 2426  
 Db 186 TGATCGGCCCTCTGGGAGGGTATCATGCCAGCAAGCAAGCTCATAGGTGATCGA 245

QY 2427 GGAGGTGTATAATCATGAGGCCAACGGGGCTTATCTTGAGGGAGATCCACCTCGT 2486  
 Db 246 GGAGGTGTATAATCATGAGGCCAACGGGGCTTATCTTGAGGGAGATCCACCTCGT 305

QY 2487 GCTCAACTGCATGGGGAACAGCTTGGAGTGCAGATTTCGTTGGCATATTTCG 2546  
 Db 306 GCTCAACTGCATGGGGAACAGCTTGGAGTGCAGATTTCGTTGGCATATTTCG 365

QY 2547 CCACAAGTTACCCGACCAAGAGACCTTCATGAAGCGGCCAGGGCAGGTAAAGCAGAT 2606  
 Db 366 CCACAAGTTACCCGACCAAGAGACCTTCATGAAGCGGCCAGGGCAGGTAAAGCAGAT 425

QY 2607 GTTGCACTCCGCTGCAGGCCATTCTGAAGAGATCGATGGATATGCCATGTTGGATAGAAC 2666  
 Db 426 GTTGCACTCCGCTGCAGGCCATTCTGAAGAGATCGATGGATATGCCATGTTGGATAGAAC 485

QY 2667 TCGGCTGAGGCCATTCTGAAGAGATCGATGGATATGCCATGTTGGATAGAAC 2726  
 Db 486 TCGGCTGAGGCCATTCTGAAGAGATCGATGGATATGCCATGTTGGATAGAAC 545

QY 2727 CCAGAACGAGTCACGGAGATATGCTATTGAGGATATGCCATGTTGGATAGAAC 2786

Db 546 CCAGAACGAGTCACGGAGATATGCTATTGAGGATATGCCATGTTGGATAGAAC 605  
 QY 2787 GATTAATGGATCGCTCAGGAGTATTCCATGGCGCCACAGGAACAGAAATTCCC 2846  
 Db 606 GATTAATGGATCGCTCAGGAGTATTCCATGGCGCCACAGGAACAGAAATTCCC 665

RESULT 11  
 US-10-369-493-38940  
 ; Sequence 38940, Application US/10369493  
 ; Publication No. US20030233675A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Goldman, Barry S.  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 ; CURRENT APPLICATION NUMBER: US/10/369, 493  
 ; PRIORITY FILING DATE: 2003-02-28  
 ; PRIORITY FILING DATE: 2002-02-21  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO 38940  
 ; LENGTH: 720  
 ; TYPE: DNA  
 ; ORGANISM: Agrobacterium tumefaciens  
 ; US-10-369-493-38940

Query Match 22.4%; Score 711.8; DB 16; Length 720;  
 Best Local Similarity 99.7%; Pred. No. 1.9e-121;  
 Matches 713; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2187 CCTGCATCTAATTCGGTCCAACCTGCAAGGAAAGACGGACGACGGGATAGCTCTTGC 2246  
 Db 6 CCTGCATCTAATTCGGTCCAACCTGCAAGGAAAGACGGACGACGGGATAGCTCTTGC 65

QY 2247 CCAGCAGACAGGGCTCCAGTCTCTTGCGTCTGATCGGTCCAATCGTGTCTCAACTATC 2306  
 Db 66 CCAGCAGACAGGGCTCCAGTCTCTTGCGTCTGATCGGTCCAATCGTGTCTCAACTATC 125

QY 2307 AACCGGAAGGGGACGACCAACAGTGGAAAGAACTGAAGAACGAGCGGTCTCTACCTTGA 2366  
 Db 126 AACCGGAAGGGGACGACCAACAGTGGAAAGAACGAGCGGTCTCTACCTTGA 185

QY 2367 TGATCGGCCCTCTGGGAGGGTATCATGCCAGCAAGCAAGCTCATAGGTGATCGA 2426  
 Db 186 TGATCGGCCCTCTGGGAGGGTATCATGCCAGCAAGCAAGCTCATAGGTGATCGA 245

QY 2427 GGAGGTGTATAATCATGAGGCCAACGGGGCTTATCTTGAGGGAGATCCACCTCGT 2486  
 Db 246 GGAGGTGTATAATCATGAGGCCAACGGGGCTTATCTTGAGGGAGATCCACCTCGT 305

QY 2487 GCTCAACTGCATGGGGAACAGCTTGGAGTGCAGATTTCGTTGGCATATTTCG 2546  
 Db 306 GCTCAACTGCATGGGGAACAGCTTGGAGTGCAGATTTCGTTGGCATATTTCG 365

QY 2547 CCACAAGTTACCCGACCAAGAGACCTTCATGAAGCGGCCAGGGCAGGTAAAGCAGAT 2606  
 Db 366 CCACAAGTTACCCGACCAAGAGACCTTCATGAAGCGGCCAGGGCAGGTAAAGCAGAT 425

QY 2607 GTTGCACTCCGCTGCAGGCCATTCTGAAGAGATCGATGGATATGCCATGTTGGATAGAAC 2666  
 Db 426 GTTGCACTCCGCTGCAGGCCATTCTGAAGAGATCGATGGATATGCCATGTTGGATAGAAC 485

QY 2667 TCGGCTGAGGCCATTCTGAAGAGATCGATGGATATGCCATGTTGGATAGAAC 2726  
 Db 486 TCGGCTGAGGCCATTCTGAAGAGATCGATGGATATGCCATGTTGGATAGAAC 545

QY 2727 CCAGAACGAGTCACGGAGATATGCTATTGAGGATATGCCATGTTGGATAGAAC 2786

RESULT 12  
US-10-369-493-38964  
; Sequence 38964, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369, 493  
; CURRENT FILING DATE: 2003-02-28  
; PRIORITY NUMBER: US 60/360, 039  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 38964  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Agrobacterium tumefaciens  
; US-10-369-493-38964

Query Match 22.4%; Score 711.8; DB 16; Length 720;  
Best Local Similarity 99.7%; Pred. No. 1.9e-121;  
Matches 713; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2187 CCTGCATCTAATTTCGGTCCAACTTGCACAGGAAGACGACGGGATACTCTTG 2246  
Db 6 CCTGCATCTAATTTCGGTCCAACTTGCACAGGAAGACGACGGGATACTCTTG 65

QY 2247 CCAGCAGACAGGGCTCCAGTGGTCCAACTTGCACAGGAAGACGACGGGATACTCTTG 2306  
Db 6 CCTGCATCTAATTTCGGTCCAACTTGCACAGGAAGACGACGGGATACTCTTG 125

QY 2307 AACCGGAAGGGACGACCAACAGTGGAAACTGGAAGAACGACGGGCTCTACCTTGA 2366  
Db 126 AACCGGAAGGGACGACCAACAGTGGAAACTGGAAGAACGACGGGCTCTACCTTGA 185

QY 2367 TGATCGGCCCTCTGGTGGAGGGTATCATCGCAGCCAGCAAGCTCATCATAGGCTGTG 2426  
Db 186 TGATCGGCCCTCTGGTGGAGGGTATCATCGCAGCCAGCAAGCTCATCATAGGCTGTG 245

QY 2427 GGAGGTGTATAATCATGAGGCCAACGGCGGCTTATTCTGAGGGAGGTCCACCTCGT 2486  
Db 246 GGAGGTGTATAATCATGAGGCCAACGGCGGCTTATTCTGAGGGAGGTCCACCTCGT 305

QY 2487 GCTCAACTGCACTGGCGCGAACAGCTATGGAGTGCAGATTTCGTTGCGATATTTCG 2546  
Db 306 GCTCAACTGCACTGGCGCGAACAGCTATGGAGTGCAGATTTCGTTGCGATATTTCG 365

QY 2547 CCACAAAGTTACCCGACCAGACACCTCATGAAAGGGCCAAGGCCAGAGTTAACGAG 2606  
Db 366 CCACAAAGTTACCCGACCAGACACCTCATGAAAGGGCCAAGGCCAGAGTTAACGAG 425

QY 2607 GTGACCCCCGCTGCAGGCCATTCTGAAAGAGATCGATGGATATGCCATGTRGTTGCT 2666

RESULT 13  
US-10-369-493-38966  
; Sequence 38966, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369, 493  
; CURRENT FILING DATE: 2003-02-28  
; PRIORITY NUMBER: US 60/360, 039  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 38966  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Agrobacterium tumefaciens  
; US-10-369-493-38966

Query Match 22.4%; Score 711.8; DB 16; Length 720;  
Best Local Similarity 99.7%; Pred. No. 1.9e-121;  
Matches 713; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2187 CCTGCATCTAATTTCGGTCCAACTTGCACAGGAAGACGACGGGATACTCTTG 2246  
Db 6 CCTGCATCTAATTTCGGTCCAACTTGCACAGGAAGACGACGGGATACTCTTG 65

QY 2247 CCAGCAGACAGGGCTCCAGTGGTCCAACTTGCACAGGAAGACGACGGGATACTCTTG 2306  
Db 6 CCTGCATCTAATTTCGGTCCAACTTGCACAGGAAGACGACGGGATACTCTTG 125

QY 2307 AACCGGAAGGGACGACCAACAGTGGAAACTGGAAGAACGACGGGCTCTACCTTGA 2366  
Db 126 AACCGGAAGGGACGACCAACAGTGGAAACTGGAAGAACGACGGGCTCTACCTTGA 185

QY 2367 TGATCGGCCCTCTGGTGGAGGGTATCATCGCAGCCAGCAAGCTCATCATAGGCTGTG 2426  
Db 186 TGATCGGCCCTCTGGTGGAGGGTATCATCGCAGCCAGCAAGCTCATCATAGGCTGTG 245

QY 2427 GGAGGTGTATAATCATGAGGCCAACGGCGGCTTATTCTGAGGGAGGTCCACCTCGT 2486  
Db 246 GGAGGTGTATAATCATGAGGCCAACGGCGGCTTATTCTGAGGGAGGTCCACCTCGT 305

QY 2487 GCTCAACTGCACTGGCGCGAACAGCTATGGAGTGCAGATTTCGTTGCGATATTTCG 2546  
Db 306 GCTCAACTGCACTGGCGCGAACAGCTATGGAGTGCAGATTTCGTTGCGATATTTCG 365

QY 2547 CCACAAAGTTACCCGACCAGACACCTCATGAAAGGGCCAAGGCCAGAGTTAACGAG 2606  
Db 366 CCACAAAGTTACCCGACCAGACACCTCATGAAAGGGCCAAGGCCAGAGTTAACGAG 425

QY 2547 CCACAAAGTTACCCGACCAGACACCTCATGAAAGGGCCAAGGCCAGAGTTAACGAG 2666

RESULT 14

US-10-465-008-1

; Sequence 1, Application US/10465008

; Publication No. US20040016016A1

; GENERAL INFORMATION:

; APPLICANT: MANKIN, LUKE S.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING PLANT PERFORMANCE

; FILE REFERENCE: 16313-0232

; CURRENT APPLICATION NUMBER: US/10/465, 008

; CURRENT FILING DATE: 2003-06-19

; PRIORITY NUMBER: 60/389, 982

; PRIORITY FILING DATE: 2002-06-19

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1997

; TYPE: DNA

; ORGANISM: Agrobacterium tumefaciens

US-10-465-008-1

Query Match 19.8%; Score 630.2; DB 16; Length 1997;

Best Local Similarity 90.2%; Pred. No. 3.4e-106;

Matches 674; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 2175 AAACCATGGACCCCTGCATCTAAATTTCGGTCCAATTTGGGCTCAACTTGACAGGAAGACGACCGC 2234

Db 681 AAACTTATGGATCTGGTCTAAATTTCGGTCCAACCTGGACAGGAAGACGACGGTGCACCGC 740

Qy 2235 GATAGCTCTGGCCAGCAGACAGGGCTCCAGTCCTTGATCGGGTCCATCGT 2294

Db 741 GGTAATGGCTGCCAGCAGACTGGGCTCCAGTCCTTGCTCGATCGGGTCCATCGT 800

Qy 2295 TCCTCAACTATCAACCGGAAGCGGACCAACAGTGGAAACTGAAAGAACGACCGC 2354

Db 801 TCCCTCAGCTGTCAACCG3AAGCGGAGACCAACAGTGGAAAGAACTGAAAGAACGACCGC 860

Qy 2355 TCTCTACCTTGATGATCGGCCCTCTGGAGGGTATCATCGCAGCCAAGCAAGCTCATCA 2414

Db 861 TCTATACTTGTGATGATCGGCCCTCTGTGAAGGGTATCATCGCAGCCAAGCTCATCA 920

Qy 2415 TAGGCTGATCGAGGGGTATAATCATGAGGCCAACGGGGCTTCTGGAGGG 2474

Db 921 AACGGCTGATGGGGAGGGTATAATATGAGGGCACGGGGCTTCTGTGAAGGG 980

Qy 2475 ATCCACCTCGTGTGCTCACTGCATGGCGAACAGCTATTGGAGTGCAGATTTCGTG 2534

Db 981 ATCTATCTCGTTGCTCAAGTGCATGGCGAACAGCTATTGGAGTGCAGATTTCGTG 1040

QY 2535 GCATATTATGCCACAAGTACCCGACCAAGAGACCTTCATGAAAGGGCCAAGGCCAG 2594

Db 1041 GCATATTATTCGOCAGGAGTAGCACAGGAGACCTTCATGAAAGGCCAG 1100

QY 2595 AGTAAGCAGATGTTGCACCCCGCTGCAGGCCATTCTATTCAAGAGTRGGTTATCT 2654

Db 1101 AGTTAACGAGATGTACGCCCTTCAGGCCTTCTATTCAAGAGTRGGTTGATCT 1160

QY 2667 TCGGTGAGGCCATTCGAAGAGATCGATGGATATCGATGCTATGCCATGTTGCT 2726

Db 486 TCGGCTGAGGCCATTCTGAAGAGATCGATGGATATCGATGCTATGCCATGTTGCT 545

QY 2727 CCAGAACAGATCACGGAGATATCTGATGGATATCGATGCTATGCCATGTTGCT 2786

Db 546 CCAGAACAGATCACGGAGATATCTGATGGATATCGATGCTATGCCATGTTGCT 605

QY 2787 GATAATGGGATCGCTCAGGAGTATTCATCCATGCCAACAGGAAGCTGAC 2846

Db 606 GATAATGGGATCGCTCAGGAGTATTCATCCATGCCAACAGGAAGCTGAC 665

QY 2847 CCAAGTTAACGCAGCCGTTCGACGGATTGACGGTCACTCGGATGTA 2901

Db 666 CCAAGTTAACGCAGCCGTTTCGACGGATTGACGGTCACTCGGATGTA 720

QY 2885 AATGTTAGGTTACGCCAGCCCTGAG 2921

Db 1401 AATGTTAGGTTACGCCAGCCCTGAG 1427

RESULT 15

US-10-369-493-38954

; Sequence 38954, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369, 493

; CURRENT FILING DATE: 2003-02-28

; PRIORITY NUMBER: US 60/360, 039

; PRIORITY FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 38954

; LENGTH: 720

; TYPE: DNA

; ORGANISM: Agrobacterium tumefaciens

US-10-369-493-38954

Query Match 19.6%; Score 624.4; DB 16; Length 720;

Best Local Similarity 92.2%; Pred. No. 2.5e-105;

Matches 658; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 2188 CTGCATCTAAATTTCGGTCCAATGTCACAGGAAGACGACGGC 2247

Db 7 CTGGCTCTAAATTTCGGTCCAATGTCACAGGAAGACGACGGC 66

Qy 2248 CAGCAGACAGGGCTCCAGTCTTCGCTGATCGGGTCCATCGTCTCTG 2307

Db 67 CAGCAGACTGGGCTCCAGTCCTTCGCTGATCGGGTCCATCGTCTCTG 126

Qy 2308 ACCGGAAGCGAACGACCAACAGTGGAAACTGAAAGAACGACGGCTCTACCTTGAT 2367

Db 127 ACCGGAAAGCGAACGACCAACAGTGGAAACTGAAAGAACGACGGCTCTACCTTGAT 186

Qy 2368 GATCGGCCTCTGGAGGGTATCATCGCAGCCAAGCAAGCTCATCGAG 2427

Db 187 GATCGGCCTCTGGAGGGTATCATCGCAGCCAAGCAAGCTCATCGAG 246

QY	2428	GAGGTATAATCATGAGGCCAACGGGGCTTATTCTTGAGGGAGGATCCACCTCGTG	2487
Db	247	GAGGTATAATTATGAGGCCAACGGGGCTTATTCTGAGGGAGGATTCCTCGTG	306
QY	2488	CTCAACTGCATGGCGCGAACAGCTTATTGGAGTCAGATTTCGTGGCATATTATCGC	2547
Db	307	CTCAAGTGCATGGCGCAAGCAGTTATTGGAGTCGGGATTCCTGGCATATTATCGC	366
QY	2548	CACAACTACCGACCAAGAGACCTTCATGAAGGGCAAGGCCAGAGTTAACAGATG	2607
Db	367	CACAGTTAGCAGAGAAGACCTTCATGAACGTTAACAGGATG	426
QY	2608	TTCACCCCGCTGCAGGCCATTCTTATTAAGAGTTATCTTGAAATGAACT	2667
Db	427	TTACGCCCTGCTGCAGGCCATTCTTATTAAGAGTTGATCTTGAAAGAGCT	486
QY	2668	CGGCTGAGGCCATTCTGAAGAGATCGATGGATATCGATGCCATTGTTGCTAGC	2727
Db	487	CGGCTGAGGCCATTCTGAAGAGATCGATGGATATCGATGCCATTGTTGCTAGC	546
QY	2728	CAGAACAGATCACATCCGATATGCTATTGAGCTTGACGCAAATGAAAGGTAGTG	2787
Db	547	CAGAACAGATCACATCCGATATGCTATTGAGCTTGACGCAAATGAAAGGTAGTG	606
QY	2788	ATTATGGATTCGCTCAGGAGATTCACTCATGGGCCAACAGGAAAGAAATCCC	2847
Db	607	ATTCAATGGATTCGCTCAGGAGATTCACTCATGGGCCAACAGGAAATCCC	666
QY	2848	CAAGTTAACCGCAGCCGTTTCGACGGATTGAAAGTCATCCGTTGGAATGTAT	2901
Db	667	CGAGTTAACCGCAGCCGTTACGACGGATTGAAAGTCATCCGTTGGAATGTAT	720

Search completed: June 10, 2004, 14:22:30  
 Job time : 5037 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

June 9, 2004, 22:11:24 ; Search time 11837 Seconds

(without alignments)  
8030.018 Million cell updates/sec

Title: US-10-072-077A-1

Perfect score: 3183

Sequence: 1.gatatatcttttttattatcca.....tatgttactagatcgaaatc 3183

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*
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#### ALIGNMENTS

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RESULT 1
CG408874
LOCUS CG408874          594 bp    DNA linear GSS 03-SEP-2003
DEFINITION Ds insertion lines Oryza sativa (japonica cultivar-group)
ACCESSION genomic, genomic survey sequence.
VERSION CG408874.1
KEYWORDS GI:34430239
SOURCE GSS.
ORGANISM Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Birrhoidae; Oryza.
REFERENCE 1 (bases 1 to 594)
AUTHORS Kim,C.M., Piao,H.L., Park,S.J., Chon,N.S., Je,B.I., Sun,B.,
        Park,S.H., Park,J.Y., Lee,E.J., Kim,M.J., Lee,J.J., Nam,M.H.,
        Bui,M.Y. and Han,C.D.
TITLE Rapid, large-scale generation of Ds transposant lines and analysis
       of Ds loci in rice
JOURNAL Unpublished (2003)
COMMENT Contact: Chang-deok Han
Division of Applied Life Science, PMBBC
Gyeongsang National University
Gazwa-dong 900, Jinju 660-701, South Korea
Tel: +82 55 751 6029
Fax: +82 55 759 9363
Email: cdhan@nongae.gsnu.ac.kr
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	250.2	7.9	594 29	CG408874 DS568
2	237.8	7.5	241 28	BZ382321 SALK 1181
C 3	216.2	6.8	628 14	CB860800 HH05GL2W
C 4	216.2	6.8	636 14	CB861695 HH02I06W

Location: chromosome 3 clone OSJNBB0020011  
 Class: transposon-tagged.  
 FEATURES source  
 Location/Qualifiers  
 /note="PCR was performed on Arabidopsis thaliana lines"  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ORIGIN

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Query Match 7.9%; Score 250.2; DB 29; Length 594;
Best Local Similarity 98.8%; Pred. No. 1.5e-36;
Matches 252; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2925 GATCGTTCAACATTTGGCAATAAAGTTCTTAGATTGATCCTGTGCCGGTCTTGCG 2984
Db 210 GATCGTTCAACATTTGGCAATAAAGTTCTTAGATTGATCCTGTGCCGGTCTTGCG 269
QY 2985 ATGATTATCATAATAATTCTGTGAATTAGCTAACATGTAAATTAACATGTATGC 3044
Db 270 ATGATTATCATAATAATTCTGTGAATTAGCTAACATGTAAATTAACATGTATGC 329
QY 3045 ATGACGTTATTATGAGATGGGTTTATGATTAGACTCCGCAATTATACATTATAC 3104
Db 330 ATGACGTTATTATGAGATGGGTTTATGATTAGACTCCGCAATTATACATTATAC 389
QY 3105 GCGATAGAAACAAATAATGGCGCGAAACTGGATAATTATCGCGCGGGTGTATCT 3164
Db 390 GCGATAGAAACAAATAATGGCGCGAAACTAGATAATTATCGCGCGGGTGTATCT 449
QY 3165 ATGTTACTAGATCGA 3179
Db 450 ATGTTACTAGATCTA 464

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RESULT 2

LOCUS	BZ382321	241 bp	DNA	linear	GSS	26-NOV-2002
DEFINITION	SALK_118148.40.60.n	Arabidopsis thaliana	genomic	clone	SALK_118148.40.60.n	genomic
ACCESSION	BZ382321					
VERSION	BZ382321.1	GI:25477222				
KEYWORDS	GSS.					
SOURCE	Arabidopsis thaliana	(thale cress)				
ORGANISM	Arabidopsis thaliana					

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 241)

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL Unpublished (2001)

COMMENT Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

FEATURES source

1. .241
  - /organism="Arabidopsis thaliana"
  - /mol\_type="genomic DNA"
  - /strain="Columbia 0"
  - /db\_xref="taxon:39947"
  - /clone\_lib="Ds insertion lines"

ORIGIN

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Query Match 7.5%; Score 237.8; DB 28; Length 241;
Best Local Similarity 99.2%; Pred. No. 3.8e-34;
Matches 239; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1285 GAACTTCATAGAGATTAGATAGATGAAATTGGGGAAACATCATGAAACAGGAAAC 1344
Db 1 GAACTTCTAGAGATTCACATAGATGAAATTGGGGAAACATCATGAAACAGGAAAC 60
QY 1345 TTAGCAAAATCGATTATCTACAAAGAACATCTAGCGTAATGAAAGTTCACTTG 1404
Db 61 TTAGCAAAATCGATTATCTACAAAGAACATCTAGCGTAATGAAAGTTCACTTG 120
QY 1405 TTGGAATGACTATGATCAAATTAGTTAATTGTCGATCATTTCTTTGA 1464
Db 121 TTGGAATGACTATGATCAAATTGTCGATCATTTCTTTGA 180
QY 1465 TTGATTAAGCTTAACTTGACGAAATGGTCTCTGTGAATAACAGAATCTTGAT 1524
Db 181 TTGATTAAGCTTAACTTGACGAAATGGTCTCTGTGAATAACAGAATCTTGAT 240
QY 1525 T 1525
Db 241 T 241

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---

RESULT 3

LOCUS	CB860800/c	628 bp	mRNA	linear	EST	22-APR-2003
DEFINITION	HH05G12w HH	Hordeum vulgare	cDNA	clone	HH05G12 5'-PRIME,	mRNA
ACCESSION	CB860800					
VERSION	CB860800.1	GI:30055359				
KEYWORDS						
SOURCE	Hordeum vulgare					
ORGANISM	Hordeum vulgare					

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum. 1 (bases 1 to 628)

REFERENCE Varshteyn,R.K., Zhang,H., Burton,R., Stein,N., Langridge,P. and Graner,A.

AUTHORS Barley ESTs from coleoptile tissue

TITLE Unpublished (2003)

JOURNAL Contact: Stein Nils

COMMENT Molecular Markers Group, Department Genbank Institute of Plant Genetics and Crop Plant Research (IPK) Correnstr. 3, 06466, Gatersleben, Germany

Correnstr. 3, 06466, Gatersleben, Germany

Tel: 039482-5522

Fax: 039482-5595

Email: stein@ipk-gatersleben.de

Insert Length: 628 Std Error: 0.00

Plate: 5 row: G column: 12

Seq primer: T7.

FEATURES source

1. .628
  - /organism="Hordeum vulgare"
  - /mol\_type="mRNA"
  - /cultivar="Sloop"
  - /db\_xref="GABI:535262"
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  - /tissue\_type="coleoptile"
  - /dev\_stage="coleoptile, 1 day old"

/lab\_host="DH10B"  
 /clone\_lib="HH"  
 /note="Vector: psport; Site 1: SalI (5-end of cDNA);  
 Site 2: NotI (3-end of cDNA); Due to the cloning system  
 used blue/white selection for recombinants is not 100 %  
 reliable. Average insert size is 1.3 kb."

## ORIGIN

Query Match						
	Best Local Similarity	Score	DB	Length	Indels	Gaps
QY	6.8%	216.2	14	628	3	3
Matches	251	Conservative	0	Mismatches	3	
Db	264	CCCGATCGTTCAACATTTGGCAATAAGTTCTTAAGATTGAATCCTGTGCCGGTCTT	2981	206		
QY	2922	CTCGATCGTTCAACATTTGGCAATAAGTTCTTAAGATTGAATCCTGTGCCGGTCTT	2981			
Db	205	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041	146		
QY	2982	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041			
Db	201	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041	142		
QY	3042	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101			
Db	145	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101	87		
QY	3102	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161			
Db	86	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161	28		
QY	3162	TCTATGTTACTAGATCG	3178			
Db	27	TCTATGTTACTAGATCG	3178	7		

## RESULT 4

Query Match						
	Best Local Similarity	Score	DB	Length	Indels	Gaps
QY	6.8%	216.2	14	636	3	3
Matches	251	Conservative	0	Mismatches	3	
Db	2922	CTCGATCGTTCAACATTTGGCAATAAGTTCTTAAGATTGAATCCTGTGCCGGTCTT	2981			
QY	2982	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041			
Db	201	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041	142		
QY	3042	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101			
Db	145	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101	87		
QY	3102	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161			
Db	82	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161	24		
QY	3162	TCTATGTTACTAGATCG	3178			
Db	23	TCTATGTTACTAGATCG	3178	7		

## RESULT 5

Query Match						
	Best Local Similarity	Score	DB	Length	Indels	Gaps
QY	6.8%	216.2	14	636	3	3
Matches	251	Conservative	0	Mismatches	3	
Db	2922	CTCGATCGTTCAACATTTGGCAATAAGTTCTTAAGATTGAATCCTGTGCCGGTCTT	2981			
QY	2982	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041			
Db	201	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041	142		
QY	3042	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101			
Db	145	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101	87		
QY	3102	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161			
Db	82	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161	24		
QY	3162	TCTATGTTACTAGATCG	3178			
Db	23	TCTATGTTACTAGATCG	3178	7		

## RESULT 6

Query Match						
	Best Local Similarity	Score	DB	Length	Indels	Gaps
QY	6.8%	216.2	14	636	3	3
Matches	251	Conservative	0	Mismatches	3	
Db	2922	CTCGATCGTTCAACATTTGGCAATAAGTTCTTAAGATTGAATCCTGTGCCGGTCTT	2981			
QY	2982	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041			
Db	201	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041	142		
QY	3042	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101			
Db	145	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101	87		
QY	3102	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161			
Db	82	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161	24		
QY	3162	TCTATGTTACTAGATCG	3178			
Db	23	TCTATGTTACTAGATCG	3178	7		

## RESULT 7

Query Match						
	Best Local Similarity	Score	DB	Length	Indels	Gaps
QY	6.8%	216.2	14	636	3	3
Matches	251	Conservative	0	Mismatches	3	
Db	2922	CTCGATCGTTCAACATTTGGCAATAAGTTCTTAAGATTGAATCCTGTGCCGGTCTT	2981			
QY	2982	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041			
Db	201	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041	142		
QY	3042	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101			
Db	145	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101	87		
QY	3102	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161			
Db	82	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161	24		
QY	3162	TCTATGTTACTAGATCG	3178			
Db	23	TCTATGTTACTAGATCG	3178	7		

## RESULT 8

Query Match						
	Best Local Similarity	Score	DB	Length	Indels	Gaps
QY	6.8%	216.2	14	636	3	3
Matches	251	Conservative	0	Mismatches	3	
Db	2922	CTCGATCGTTCAACATTTGGCAATAAGTTCTTAAGATTGAATCCTGTGCCGGTCTT	2981			
QY	2982	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041			
Db	201	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041	142		
QY	3042	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101			
Db	145	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101	87		
QY	3102	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161			
Db	82	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161	24		
QY	3162	TCTATGTTACTAGATCG	3178			
Db	23	TCTATGTTACTAGATCG	3178	7		

## RESULT 9

Query Match						
	Best Local Similarity	Score	DB	Length	Indels	Gaps
QY	6.8%	216.2	14	636	3	3
Matches	251	Conservative	0	Mismatches	3	
Db	2922	CTCGATCGTTCAACATTTGGCAATAAGTTCTTAAGATTGAATCCTGTGCCGGTCTT	2981			
QY	2982	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041			
Db	201	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041	142		
QY	3042	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101			
Db	145	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101	87		
QY	3102	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161			
Db	82	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161	24		
QY	3162	TCTATGTTACTAGATCG	3178			
Db	23	TCTATGTTACTAGATCG	3178	7		

## RESULT 10

Query Match						
	Best Local Similarity	Score	DB	Length	Indels	Gaps
QY	6.8%	216.2	14	636	3	3
Matches	251	Conservative	0	Mismatches	3	
Db	2922	CTCGATCGTTCAACATTTGGCAATAAGTTCTTAAGATTGAATCCTGTGCCGGTCTT	2981			
QY	2982	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041			
Db	201	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041	142		
QY	3042	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101			
Db	145	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101	87		
QY	3102	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161			
Db	82	TACGGATAGAACAAATATGGCGCGCAACTGGGATAATTATCGGCCGGTGTCA	3161	24		
QY	3162	TCTATGTTACTAGATCG	3178			
Db	23	TCTATGTTACTAGATCG	3178	7		

## RESULT 11

Query Match						
	Best Local Similarity	Score	DB	Length	Indels	Gaps
QY	6.8%	216.2	14	636	3	3
Matches	251	Conservative	0	Mismatches	3	
Db	2922	CTCGATCGTTCAACATTTGGCAATAAGTTCTTAAGATTGAATCCTGTGCCGGTCTT	2981			
QY	2982	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041			
Db	201	GCGATGATTATCATATAATTCTGTGAAATTACGTTAACATGTAA	3041	142		
QY	3042	TGCATGACGTTATTATGAGATGGTTATTGATTAGACTCCGCAATTACATTAA	3101			
Db						

directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

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Query Match      5.3%; Score 168.6; DB 14; Length 311;
Best Local Similarity 89.6%; Pred. No. 2.8e-21;
Matches 180; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```

Query Match	6.6%	Score 210;	DB 28;	Length 286;
Best Local Similarity	85.7%	Pred. No.	5.5e-29;	
Matches	245;	Conservative	0;	Mismatches 40;
Indels	1;	Gaps 1;		
Db	66	CCGATCGTCAACATTGGCAATAAGTTCTTAAGATGAATCCGTGTCGGTCTT	125	
QY	1140	GTTATCACTTCAGCAAATATGATTGGTTAAGCCAAATGCAATTTCGTACGTAC 1199		
Db	1	GTTATCACTTCAGCAAATATGATTGGTTAAGCTTCAATTCATACTACAGGC-TA	1258	
QY	1200	CCTCTTGTCGCTAATGATTATTCAATATTCTTACTACAGAGC-TA	1258	
Db	61	CCTCTGGGACTAATGATGATTCAATATTCTTACATTCCCTATCTGCCAGGGTA	120	
QY	1259	CATTATATGTTCTAATGACAGGGAACTTCTATAGAGATTCAGATAGATAATG	1318	
Db	121	CCTTATATGGATTCTAATGACAGGGAACTTCTGTAGATATTACATAGATAATG	180	
QY	1319	GTGGGAAACATCATGAACTTTAGCAAATCATATCGATTATCTACAAGA	1378	
Db	181	GTGGGAAACATCATGAACTTTAGTCCATCATCCACCTCCACAACA	240	
QY	1379	ATACTTAGCGTAATGAGTTCACTTGTGTAATGGACTATGATTG	1424	
Db	241	ATACTTACCCTAACGAGCCCCACTTGTGCGAATCGCTATGATTG	286	
RESULT 6				
LOCUS	CF307942	311 bp mRNA linear EST 15-AUG-2003		
DEFINITION	ABF--01-J01.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cdNA clone ABF--01-J01, mRNA sequence.			
ACCESSION	CF307942			
VERSION	CF307942.1	GI:33679703		
KEYWORDS	EST.			
SOURCE	Oryza sativa			
ORGANISM	Oryza sativa			
REFERENCE	1 (bases 1 to 311)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.		
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.			
TITLE	Large-scale Sequencing Analysis of Rice ESTs			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Haitao Dong, Debao Li Bioinformatics and Gene Network Research Group Zhejiang University Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China Tel: 0086-571-86892051 Fax: 0086-571-86961525 Email: webmaster@estarray.org, URL: http://www.estarray.org Seq primer: M13 forward primer.			
FEATURES	source	Location/Qualifiers		
FEATURES	source	1. .584 /organism="Oryza sativa" /mol_type="mRNA" /db_xref="taxon:4530" /clone="S104H12" /tissue_type="Stem" /dev_stage="3-5 leaf stage" /clone_lib="Stem library from Oryza sativa (3-5 leaf stage)" /note="Vector: psport2"		
ORIGIN	Query Match	5.3%; Score 168; DB 12; Length 584;		
	Best local Similarity	87.6%; Pred. No. 3.1e-21;		
	Matches	183; Conservative 0; Mismatches 26; Indels 0; Gaps 0;		
Db	2982	CTCGATCGTCAAACATTGGCAATAAGTTCTTAAGATGAATCCGTGTCGGTCTT	2981	
QY	126	GCGATCGTCAAACATTGGCAATAAGTTCTTAAGATGAATCCGTGTCGGTCTT	185	
QY	3042	TGCATGACGTTATTGAGATGGTTTATGATTAGAGTCCCACATTACATTAA	3101	
Db	186	TGCATGACGTTATTGAGATGGTTTATGATTAGAGTCCCACATTACATTAA	245	
QY	3102	TACCGATAGAAAACAAATA	3122	
Db	246	AAAAAAA	266	
RESULT 7				
LOCUS	BI807352	584 bp mRNA linear EST 02-OCT-2001		
DEFINITION	S104H12 Stem library from Oryza sativa (3-5 leaf stage) Oryza sativa cdNA clone S104H12, mRNA sequence.			
ACCESSION	BI807352			
VERSION	BI807352.1	GI:15854556		
KEYWORDS	EST.			
SOURCE	Oryza sativa			
ORGANISM	Oryza sativa			
REFERENCE	1 (bases 1 to 584)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.		
AUTHORS	Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.			
TITLE	A Gene Expression Screen in Oryza sativa			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Haitao Dong, Debao Li Bioinformatics and Gene Network Research Group Zhejiang University Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China Tel: 0086-571-86892051 Fax: 0086-571-86961525 Email: webmaster@estarray.org, URL: http://www.estarray.org Seq primer: M13 forward primer.			
FEATURES	source	Location/Qualifiers		
FEATURES	source	1. .584 /organism="Oryza sativa" /mol_type="mRNA" /db_xref="taxon:4530" /clone="S104H12" /tissue_type="Stem" /dev_stage="3-5 leaf stage" /clone_lib="Stem library from Oryza sativa (3-5 leaf stage)" /note="Vector: psport2"		
ORIGIN	Query Match	5.3%; Score 168; DB 12; Length 584;		
	Best local Similarity	87.6%; Pred. No. 3.1e-21;		
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Db	2936	CATTGGCAATAAGTTCTAAGATGAACTCCTGTTGCCGTCTGGCATGATTATCAT	2995	
QY	313	CAGGGGGCGGAATCACTAGTGTGAATCCTGTTGCCGTCTGGCATGATTATCAT	372	
QY	2996	ATAATTCTGTTGAATTACGTTAAGCATGTAATAATTACATGTAATGCACTGACGTTATT	3055	
Db	373	ATAATTCTGTTGAATTACGTTAAGCATGTAATAATTACATGTAATGCACTGACGTTATT	432	

QY	3 056 TATGAGATGGGTTTATGATTAGAGTCCCCTAATTACATTAATACGGATAGAAA	3115	DEFINITION	EST758506 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NBMCX34 3'
Db	4 33 TATGAGATGGGTTTATGATTAGAGTCCCCTAATTACATTAATACGGATAGAAA	492	LOCUS	normalized, full-length Nicotiana benthamiana cDNA clone NBMCX34 3'
QY	3 116 CAAATATGGCCGCCAAACTGGGATAAT	3144	DEFINITION	end, mRNA sequence.
Db	4 93 ACAATATAGGCCCAAATAGGATAAT	521	ACCESSION	CK295792
			VERSION	CK295792.1 GI:39880533
			KEYWORDS	EST.
			SOURCE	Nicotiana benthamiana
			ORGANISM	Nicotiana benthamiana
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
REFERENCE	CF308453	547 bp	mRNA	linear EST 15-AUG-2003
DEFINITION	ABF--02-E14.91 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--02-E14, mRNA sequence.			
ACCESSION	CF308453			
VERSION	CF308453.1			
KEYWORDS	EST.			
SOURCE	Oryza sativa			
ORGANISM	Oryza sativa			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
ERHARTOIDEAE; ORYZEAE; Oryza.				
1 (bases 1 to 547)				
REF ID: CF308453				
AUTHORS	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,			
TITLE	Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.			
JOURNAL	Large-scale Sequencing Analysis of Rice ESTs			
COMMENT	Unpublished (2003)			
CONTACT	Contact: Nahm, B.H.			
FEATURES	Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University			
FEATURES	Location/Qualifiers			
source	Email: bhnahn@gbio.com, bhnahn@bio.myongji.ac.kr.			
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FEATURES	CDNA library (ABF)"			
/note="Vector: PCR4-TOPO; Site_1: ECORI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."	/note="Vector: PCR4-TOPO; Site_1: ECORI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."			
ORIGIN	Query Match			
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzae; Oryza.

REFERENCE  
 1 (bases 1 to 688)

AUTHORS  
 Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X.,  
 Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.

TITLE  
 A Gene Expression Screen in *Oryza sativa*

JOURNAL  
 Unpublished (2001)

COMMENT  
 Contact: Haitao Dong, Debao Li  
 Bioinformatics and Gene Network Research Group  
 Zhejiang University  
 Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China  
 Tel: 0086-571-86892051  
 Fax: 0086-571-86961525  
 Email: webmaster@estarray.org, URL: <http://www.estarray.org>

FEATURES  
 source

LOCATION/QUALIFIERS  
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 /organism="Oryza sativa"  
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 /clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; Leaf was dried for 2 hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

ORIGIN  
 Seq primer: M13 forward primer.  
 Location/Qualifiers

ORIGIN  
 Query Match 4.7%; Score 150; DB 12; Length 688;  
 Best Local Similarity 93.8%; Pred. No. 6.8e-18;  
 Matches 167; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 2968 CTGGTGCAGGCTTGCGATGATTACATAATTCTGTGAATTACGTTAACATGTAA 3027  
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QY 3028 TAATTAACATGTAATGCATGACGTTATTGAGATGGGTTTATGATTAGTAGTCCGC 3087  
 Db 563 TAATTAACATGTAATGCATGACGTTATTGAGATGGGTTTATGATTAGTCGGC- 505

QY 3088 AATTATACATTAATACGGATAGAAACAAATAATGGGATAAATT 3145  
 Db 504 AATTATACATTAATACGGATAGAAACAAATAATAGCGGCAACTAGGATAAAT 447

RESULT 11

LOCUS CF308452 ABF3-02-E14.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) *Oryza sativa* CDNA clone ABF-02-E14, mRNA sequence.

DEFINITION 222 bp mRNA linear EST 15-AUG-2003

ACCESSION CF308452.1 GI:33680213

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 130)

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shimn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL Unpublished (2001)

COMMENT  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

CLASS: TDNA tagged.

FEATURES  
 source

LOCATION/QUALIFIERS  
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FEATURES  
 source

LOCATION/QUALIFIERS  
 1. .222



RESULT 14  
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DEFINITION CS0DF005Y01B 3'-PRIME, mRNA sequence.  
ACCESSION AL565455  
VERSION AL565455.2 GI:30549492  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Butheria; Primates; Catarhini; Hominidae; Homo.  
1 (bases 1 to 1201)  
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
COMMENT On Feb 16, 2001 this sequence version replaced gi:12916848.  
Contact: Genoscope  
Genoscope - Centre National de Séquençage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 9232.f. For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DF005BH09NP1&cluster=9232.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Parady Avenue Genoscope sequence ID : CS0DF005BH09NP1.  
FEATURES source  
1. .1201  
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vector. Library was not normalized."  
ORIGIN  
Query Match 3.6%; Score 113.6; DB 9; Length 1201;  
Best Local Similarity 35.6%; Pred. No. 3.7e-11;  
Matches 315; Conservative 134; Mismatches 433; Indels 2; Gaps 2;  
QY 1009 AAGATCCAAGAATATGTCCTACTCTTGTAAAGAACTAACTATCACTAA 1068  
Db 320 ATATACCAAAACAAACTCTTACTTCCCTGTGGTAGGTGCCACAGAATGAGATAAG 379  
QY 1069 TAAATAATTCTAATCATATAATTGCAAGTTTGTCAATTGTAATTAG 1128  
Db 380 CAATAAAATGCATATTCACTGCAATGTGAAGTAGAAGGGTATATCCTATATAWAT 439  
QY 1129 TATTTAGACGGTATCACTCAGCAAATATGATTAAAGTCCAAATGCAATT 1188  
Db 440 AWATAWATAWATAWATAWATAWATAWATAWATAWATAWATAWATAWATAWAT 499  
QY 1189 TCGTAGCTATCCCTCTGTCGTCATAATGATTATTCAATATTCTTATTATTCCCTAAC 1248  
Db 500 AWATAWATAWATAT-AWATAWATAWATAWATAWATAWATAWATAWATAWATAWA 558  
QY 1249 TAGAGAGCTACATTATGATTCTAATGACAGGAACCTTCATAGAGATTGAGATA 1308  
Db 559 TAWATAWATAWATAWATAWATAWATAWATAWATAWATAWATAWATAWATAWA 618  
QY 1309 GATGAATGGTGGAAACATCATGGACAGGAACCTTCAATGAAATATCGATTAT 1368  
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RESULT 15  
CG753083 CG753083 1896 bp DNA linear GSS 24-OCT-2003  
LOCUS CG753083 P048-1-C01.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,  
DEFINITION genomic survey sequence.  
ACCESSION CG753083.1 GI:37977199  
VERSION CG753083  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
REFERENCE 1 (bases 1 to 1896)  
AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,  
Buntjer,J., van der Meulen,M. and Sommer,R.J.  
TITLE An integrated physical and genetic map of the nematode *Pristionchus pacificus*  
JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)  
MEDLINE 22835951  
PUBMED 12884007  
COMMENT Contact: Sommer R.J.  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
Class: BAC ends.  
FEATURES source  
1. .1896  
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the genomic DNA with *ECORI* and cloning into the BAC vector."

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Job time : 11847 secs

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